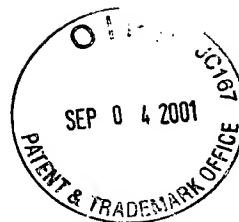


Amot "D"  
~~#123~~



24737-1906C

SEQUENCE LISTING

<110> Kalyanaraman Ramnarayan  
Edward T. Maggio  
P. Patrick Hess

<120> Use of Computationally Derived Protein  
Structures of Genetic Polymorphisms in Pharmacogenomics for  
Drug Design and Clinical Applications

RECEIVED

SEP 06 2001

TECH CENTER 1600/2900

<130> 24737-1906C

<140> Unassigned

<141> 2000-11-10

<150> 09/438,566

<151> 1999-11-10

<150> 24737-1906B

<151> 2000-11-01

<160> 118

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified Hepatitis C Virus NS3 Protease Inhibitor  
Peptide

<221> ACETYLTATION

<222> 1

<221> MOD\_RES

<222> 2

<223> D-glutamic acid

<221> MOD\_RES

<222> 5

<223> beta-cyclohexylalanine

<300>

<301> Ingallinella, P., Altamura, S., Bianchi, E., Talia

<302> Potent Peptide Inhibitors Of Human Hepatitis C Vir

<303> Biochemistry

<304> 37

<305> 25

<306> 8906-8914

<307> 1998-06-23

<400> 1

Asp Xaa Leu Ile Xaa Cys  
1 5

<210> 2

<211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Modified Hepatitis C Virus NS3 Protease Inhibitor Peptide

<221> ACETYLTATION  
 <222> 1

<221> MOD\_RES  
 <222> 5  
 <223> beta-cyclohexylalanine

<300>  
 <301> Ingallinella, P., Altamura, S., Bianchi, E., Talia  
 <302> Potent Peptide Inhibitors Of Human Hepatitis C Vir  
 <303> Biochemistry  
 <304> 37  
 <305> 25  
 <306> 8906-8914  
 <307> 1998-06-23

<400> 2  
 Asp Glu Leu Ile Xaa Cys  
 1 5

<210> 3  
 <211> 1045  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> Protease

<221> CDS  
 <222> (298)...(1045)  
 <223> Portion of Reverse Transcriptase

<400> 3  
 cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly  
 1 5 10 15  
 ggc caa cta aaa gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30  
 tta gaa gaa atg agt tta cca ggg aaa tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata ctc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile  
 50 55 60  
 gaa atc tgt gga cat aaa gct ata ggc aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

|   |      |
|---|------|
| cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act | 288  |
| Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr |      |
| 85 90 95  |      |
| tta aat ttg ccc att agt cct att gaa act gta cca gta aaa tta aag | 336  |
| Leu Asn Leu Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gag aat cca tac aat act cca ata ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe |      |
| 145 150 155 160   |      |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc | 528  |
| Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aga aca caa gac ttc tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cac ccc gca ggg tta aaa cag aaa aaa tca gta aca ata ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa ggc ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt aga aat aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat cag tac aac gtg ctc cca cag gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttt caa agt agc atg aca aga aty tta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Arg Xaa Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta | 864  |
| Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gaa ata gga cag cat aga gca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga gga cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat | 960  |
| Arg Gly His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |

aaa tgg aca gta cag cct ata aag ttg cca gaa aaa g 1045  
 Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys  
 340 345

<210> 4  
 <211> 1046  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1046)  
 <223> Portion of HIV Reverse Transcriptase

<400> 4  
 cct cag atc act ctt tgg caa cga ccc ctt gtc aca ata aag ata gga 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
 1 5 10 15  
 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
 20 25 30  
 gtt gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144  
 Val Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta aga cag tat gag caa ata gcc gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile Ala Val  
 50 55 60  
 gaa aty tgt gga cat aga gct atg ggt aca gta tta gta gga cct aca 240  
 Glu Xaa Cys Gly His Arg Ala Met Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80  
 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
 130 135 140  
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175



```

aga gaa ctt aat aag aga act caa gac ttc tgg gag gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
      180      185      190

ata cca cat cca gca ggg tta aaa aag aat aaa tca ata aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ile Thr Val Leu
      195      200      205

gat gtg ggt gat gca tat ttt tca gtt ccc tta tgt gaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Cys Glu Asp Phe Arg
      210      215      220

aag tat act gca ttt acc ata cct agt gta aac aat gag act cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly
      225      230      235      240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga ttc acc      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Phe Thr
      245      250      255

agc ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ser Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
      260      265      270

caa aat cca gag ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
      275      280      285

gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
      290      295      300

aga caa tat ctg tgg aag tgg gga ttt tgc aca cca gaa caa aar cat      960
Arg Gln Tyr Leu Trp Lys Trp Gly Phe Cys Thr Pro Glu Gln Lys His
      305      310      315      320

cag aaa gaa cct cct ttc ctt tgg atg ggt tat gaa ctc cat ccc gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325      330      335

aaa tgg aca gta caa cct ata gtg ctg cca gac aaa ga      1046
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys
      340      345

```

```

<210> 5
<211> 1104
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1) ... (297)
<223> HIV Protease

<221> CDS
<222> (298) ... (1104)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 5
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag rta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Xaa Gly
  1              5              10              15

```

|   |     |
|---|-----|
| ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca ata<br>Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile<br>20 25 30        | 96  |
| ata gaa gac ata act ttg cca gga aga tgg aca cca aaa atg ata ggg<br>Ile Glu Asp Ile Thr Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata<br>Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile<br>50 55 60        | 192 |
| gaa atc tgc gga cat aaa rtt ata agt aca gta ttg gta gga cct aca<br>Glu Ile Cys Gly His Lys Xaa Ile Ser Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cca ata aac ata gtt gga aga aat ctg atg act cag att ggt tgc act<br>Pro Ile Asn Ile Val Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gtc aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aag gca tta gta gaa att tgt mca gaa ctg gaa atg gat gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Xaa Glu Leu Glu Met Asp Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat ccg tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aac aaa aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca att ccc tta tgt gaa gac ttc aga<br>Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Cys Glu Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |

cag aat cca gaa atg gtc atc tat caa tac gtg gat gat ttg tat gta 864  
Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val  
275 280 285

gga tct gac tta gaa ata gag cag cat aga aca aaa ata gat gaa ctg 912  
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu  
290 295 300

aga caa tat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat 960  
Arg Gln Tyr Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His  
305 310 315 320

cag aca gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
Gln Thr Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365

<210> 6  
<211> 1116  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease

<221> CDS  
<222> (298)...(1116)  
<223> Portion of HIV Reverse Transcriptase

<400> 6  
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48  
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30

tta gaa gat atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
35 40 45

gga att gga ggt ttt atc aaa gta agg cag tat gat caa ata ctc ata 192  
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile  
50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240  
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
65 70 75 80

cct gtc aac ata att gga agg aat ctg ttg act cag att ggt tgc act 288  
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336  |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gag gag<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta aaa aag aaa aag tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aag tac act gca ttt act ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg ata aaa atc tta gag cct ttc aga aaa<br>Ala Ile Phe Gln Ser Ser Met Ile Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac atg gtc atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata gga cag cac aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aag aaa cat<br>Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata aag ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |

```

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg
Ile Tyr Pro Gly
      370

<210> 7
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 7
cct cag atc act ctt tgg caa cga ccc ctt gtc aca ata aar ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gag gaa atn aat tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Xaa Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val
      50                      55                      60

gaa aty tgt gga cat aar gct ata ggt aca gta tta gta gga cct aca      240
Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

ccc gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

ccg gga atg gat ggc ccc aaa gtt aaa cat ggc cct ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys His Gly Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aag cct tta gtt gaa att tgt aca gaa atg gga aaa gaa ggg      432
Lys Ile Lys Pro Leu Val Glu Ile Cys Thr Glu Met Gly Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

```

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aaa aga act caa gac tty tgg gaa gtc caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc tca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat gaa gac tta gag 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Leu Glu  
 210 215 220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816  
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
 260 265 270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta 864  
 Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
 275 280 285

gga tca gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu  
 290 295 300

aga caa cat ctg ttg ggg tgg ggg ttt acc aca cca gac aaa aaa cat 960  
 Arg Gln His Leu Leu Gly Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca aca aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Thr Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tat gca ggg  
 Ile Tyr Ala Gly 1116  
 370

<210> 8  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 8
cct cag atc act ctt tgg caa cga ccc cty gtc aca gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Val Lys Ile Gly
  1                    5                    10                   15

ggg caa ata aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Ile Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
                    20                    25                   30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
                    35                    40                   45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
                    50                    55                   60

gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr
                    65                    70                   75                   80

cct gtc aat ata att gga aga aat ctg atg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
                    85                    90                   95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                    100                   105                   110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
                    115                   120                   125

aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                    130                   135                   140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                    145                   150                   155                   160

gcc ata aag aaa aaa ggc agt aac aga tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Gly Ser Asn Arg Trp Arg Lys Leu Val Asp Phe
                    165                   170                   175

aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                    180                   185                   190

ata cca cat ccc gca ggg cta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                    195                   200                   205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
                    210                   215                   220

```

```

aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa ggg tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

agc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta      912
Ser Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                               290                               295                               300

aga caa cat ctg ttg agg tgg gga tta acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gar aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tac cca ggg
Ile Tyr Pro Gly
370

```

```

<210> 9
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 9
cct cag atc act ctt tgg caa cga ccc cty gtc aaa gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Lys Val Lys Ile Gly
1                               5                               10                               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

```



|   |     |
|---|-----|
| tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata atw gga aga aat ctg ttg act cag att ggt tgc act<br>Pro Val Asn Ile Xaa Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta ata gaa att tgt aca gag atg gag aag gaa ggg<br>Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aaa act caa gay ttc tgg gaa gtt car tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aag atc tta gar cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

gga tcw gac tta gaa ata ggg caa cat aga ata aaa ata gag gaa ctg      912
Gly Xaa Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Glu Glu Leu
290                               295                               300

aga cag cat ctg tta agg tgg ggg ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp
325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gay agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                               360                               365

atc tac cca ggg
Ile Tyr Pro Gly
370

```

```

<210> 10
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

```

```

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 10
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
1                               5                               10                               15

ggg caa ata aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Ile Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atw ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly
35                               40                               45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
50                               55                               60

gaa atc tgt gga caa aaa gct ata agt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly Gln Lys Ala Ile Ser Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aat ata att gga aga aat ctg atg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
85                               90                               95

```

|   |      |
|---|------|
| tta aat ttt cct att agt cct att gaa act gta cca gta aaa taa aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys * Lys   |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |      |
| 145 150 155   |      |
| gcc ata aag aaa aaa ggc agt aac aga tgg aga aaa tta gta gat ttc | 528  |
| Ala Ile Lys Lys Lys Gly Ser Asn Arg Trp Arg Lys Leu Val Asp Phe |      |
| 160 165 170 175   |      |
| aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat ccc gca ggg cta aaa aag aaa aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly |      |
| 225 230 235   |      |
| att aga tat cag tac aat gtg ctt ccm caa gga tgg aaa ggg tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Xaa Gln Gly Trp Lys Gly Ser Pro |      |
| 240 245 250 255   |      |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac wtr gtt atc tat caa tac atg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Xaa Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| agc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta | 912  |
| Ser Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga caa cat ctg ttg agg tgg gga tta acc aca cca gac aaa aaa cat | 960  |
| Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315   |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 320 325 330 335   |      |
| aaa tgg aca gta cag cct ata gtg ctg cca gag aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
                   355                  360                  365

att tac cca ggg 1116  
 ile tyr pro gly  
                   370

<210> 11  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 11  
 cct cag atc act ctt tgg caa cga ccc aty gtt aca ata aag ata ggg 48  
 Pro Gln ile thr leu trp gln arg pro xaa val thr ile lys ile gly  
           1                  5                  10                  15

ggg caa cta aaa raa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln leu lys xaa ala leu leu asp thr gly ala asp asp thr val  
                   20                  25                  30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata gtg 144  
 leu glu glu met asn leu pro gly arg trp lys pro lys met ile val  
           35                  40                  45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta ccc ata 192  
 Gly ile gly gly phe val lys val arg gln tyr asp gln val pro ile  
           50                  55                  60

gag atc tgt ggg cat aaa att ata ggt aca gta tta ata gga cct acc 240  
 Glu ile cys gly his lys ile ile gly thr val leu ile gly pro thr  
           65                  70                  75                  80

cct gcc aac gta att gga aga aat ctg atg act cag ctt ggt tgc act 288  
 Pro ala asn val ile gly arg asn leu met thr gln leu gly cys thr  
                   85                  90                  95

tta aat ttt ccc att agt yct att gaa act gta cca gta aaa tta aag 336  
 leu asn phe pro ile ser xaa ile glu thr val pro val lys leu lys  
           100                  105                  110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro gly met asp gly pro lys val lys gln trp pro leu thr glu glu  
           115                  120                  125

aaa ata aaa gca tta gta gaa att tgt gca gaa ctg gag aag gaa ggg 432  
 Lys ile lys ala leu val glu ile cys ala glu leu glu lys glu gly  
           130                  135                  140

aaa att tca aga att ggg cct gaa aat cca tac aat act cca ata ttt 480  
 Lys ile ser arg ile gly pro glu asn pro tyr asn thr pro ile phe  
           145                  150                  155                  160

gcc ata aag aag aaa aac agt act agg tgg aga aaa tta gta gat ttc 528  
Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe  
165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa att caa tta gga 576  
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly  
180 185 190

ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg 624  
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu  
195 200 205

gat gtg ggg gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg 672  
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg  
210 215 220

aag tac act gca ttt acc ata cct agt aca aac aat gag aca cca ggg 720  
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly  
225 230 235 240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca 768  
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255

gca ata ttc caa gat agc atg aca aaa atc tta gat ccc ttt aga aag 816  
Ala Ile Phe Gln Asp Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys  
260 265 270

aaa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta 864  
Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val  
275 280 285

gga tct gac yta gaa ata gag cag cat aga gca aaa ata gag gaa ctg 912  
Gly Ser Asp Xaa Glu Ile Glu Gln His Arg Ala Lys Ile Glu Glu Leu  
290 295 300

aga gaa tat ctg tta aag tgg gga ttt ttc aca cca gag caa aaa cat 960  
Arg Glu Tyr Leu Leu Lys Trp Gly Phe Phe Thr Pro Glu Gln Lys His  
305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggc tat gaa ctc cat cct gat 1008  
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335

aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act 1056  
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag 1104  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365

att tac cca ggg 1116  
Ile Tyr Pro Gly  
370

&lt;210&gt; 12

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 12
cct caa atc act ctt tgg car cga ccc tta gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg caa cta aag gaa gcc cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

cta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
             35             40             45

gga att gga ggt ttt atc aaa gta agg cag tat gat car ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
             50             55             60

gag atc tgc ggg tat aaa gct gtg ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly Tyr Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
             65             70             75             80

cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
             130            135            140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
             145            150            155            160

gcc ata aag aaa aaa gac ggt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
             180            185            190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat caa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg
             210            215            220

```

```

aag tat act gca ttc act ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                230                235                240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                245                250                255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                260                265                270

caa aat cca gac atg gtt atc tat caa tat atg gat gat ttg tat gta      864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                275                280                285

ggc tct gac tta gaa aya ggg cag cat aga rca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu
290                295                300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                310                315                320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                325                330                335

aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr
                340                345                350

gtc aat gac ata cag aag cta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                355                360                365

att tat gca ggg
Ile Tyr Ala Gly
370
1116

<210> 13
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 13
cct cag atc act ctt tgg caa cga ccc aty gtc aac ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Asn Ile Lys Val Gly
1                5                10                15

ggg caa cta arg gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Xaa Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                20                25                30

```

|                            |                    |                    |                    |                    |                    |                    |            |     |
|----------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|-----|
| tta gaa gac<br>Leu Glu Asp | ata gat<br>Ile Asp | ttg cca<br>Leu Pro | gga aga<br>Gly Arg | tgg aga<br>Trp Arg | cca aga<br>Pro Arg | atg ata<br>Met Ile | ggg<br>Gly | 144 |
| 35                         |                    |                    | 40                 |                    | 45                 |                    |            |     |
| gga att gga<br>Gly Ile Gly | ggt ttt<br>Gly Phe | gtc aaa<br>Val Lys | gta aag<br>Val Lys | cag tat<br>Gln Tyr | gat cag<br>Asp Gln | ata ccc<br>Ile Pro | ata<br>Ile | 192 |
| 50                         |                    | 55                 |                    |                    | 60                 |                    |            |     |
| gaa ata tgt<br>Glu Ile Cys | gga cat<br>Gly His | aaa gtt<br>Lys Val | ata ggt<br>Ile Gly | aca gta<br>Thr Val | tta gta<br>Leu Val | gga cct<br>Gly Pro | acg<br>Thr | 240 |
| 65                         |                    | 70                 |                    | 75                 |                    |                    | 80         |     |
| cct gcc aac<br>Pro Ala Asn | ata att<br>Ile Ile | gga aga<br>Gly Arg | aat ctg<br>Asn Leu | ttg act<br>Leu Thr | cag att<br>Gln Ile | ggg tgc<br>Gly Cys | act<br>Thr | 288 |
|                            | 85                 |                    |                    | 90                 |                    | 95                 |            |     |
| tta aat ttt<br>Leu Asn Phe | ccc att<br>Pro Ile | agt cct<br>Ser Pro | att gaa<br>Ile Glu | act gta<br>Thr Val | cca gta<br>Pro Val | aaa tta<br>Lys Leu | aaa<br>Lys | 336 |
|                            | 100                |                    | 105                |                    |                    | 110                |            |     |
| cca gga atg<br>Pro Gly Met | gat ggc<br>Asp Gly | cca aaa<br>Pro Lys | gtt aaa<br>Val Lys | caa tgg<br>Gln Trp | cca ttg<br>Pro Leu | aca gaa<br>Thr Glu | gaa<br>Glu | 384 |
| 115                        |                    |                    | 120                |                    | 125                |                    |            |     |
| aag ata aaa<br>Lys Ile Lys | gca tta<br>Ala Leu | gta gaa<br>Val Glu | att tgt<br>Ile Cys | aca gaa<br>Thr Glu | ttg gaa<br>Leu Glu | aag gaa<br>Lys Glu | gga<br>Gly | 432 |
| 130                        |                    | 135                |                    | 140                |                    |                    |            |     |
| aaa att tca<br>Lys Ile Ser | aaa att<br>Lys Ile | ggg cct<br>Gly Pro | gaa aat<br>Glu Asn | cca tac<br>Pro Tyr | aat act<br>Asn Thr | cca gta<br>Pro Val | ttt<br>Phe | 480 |
| 145                        |                    | 150                |                    | 155                |                    |                    | 160        |     |
| gcc ata aag<br>Ala Ile Lys | aag aaa<br>Lys Lys | aac agt<br>Asn Ser | act aga<br>Thr Arg | tgg aga<br>Trp Arg | aaa tta<br>Lys Leu | gta gat<br>Val Asp | ttt<br>Phe | 528 |
|                            | 165                |                    |                    | 170                |                    | 175                |            |     |
| aga gaa ctt<br>Arg Glu Leu | aat aag<br>Asn Lys | aga act<br>Arg Thr | caa gac<br>Gln Asp | ttt tgt<br>Phe Cys | gaa gtg<br>Glu Val | caa tta<br>Gln Leu | gga<br>Gly | 576 |
|                            | 180                |                    | 185                |                    | 190                |                    |            |     |
| ata ccg cat<br>Ile Pro His | ccc gca<br>Pro Ala | ggg tta<br>Gly Leu | ara aag<br>Xaa Lys | aaa aga<br>Lys Arg | tca gta<br>Ser Val | aca gta<br>Thr Val | ctg<br>Leu | 624 |
| 195                        |                    |                    | 200                |                    | 205                |                    |            |     |
| gat gtg ggt<br>Asp Val Gly | gat gca<br>Asp Ala | tat ttt<br>Tyr Phe | tca gtt<br>Ser Val | ccc tta<br>Pro Leu | gat gaa<br>Asp Glu | gac ttc<br>Asp Phe | agg<br>Arg | 672 |
| 210                        |                    | 215                |                    | 220                |                    |                    |            |     |
| aag tat act<br>Lys Tyr Thr | gcc ttt<br>Ala Phe | acc ata<br>Thr Ile | cct agt<br>Pro Ser | ata aac<br>Ile Asn | aat gag<br>Asn Glu | aca cca<br>Thr Pro | ggg<br>Gly | 720 |
| 225                        |                    | 230                |                    | 235                |                    |                    | 240        |     |
| att aga tat<br>Ile Arg Tyr | cag tat<br>Gln Tyr | aat gtg<br>Asn Val | ctt cca<br>Leu Pro | cag gga<br>Gln Gly | tgg aaa<br>Trp Lys | gga tca<br>Gly Ser | cca<br>Pro | 768 |
|                            | 245                |                    | 250                |                    | 255                |                    |            |     |
| gca ata ttc<br>Ala Ile Phe | caa agt<br>Gln Ser | agc atg<br>Ser Met | aca aaa<br>Thr Lys | atc cta<br>Ile Leu | gag cct<br>Glu Pro | ttt aga<br>Phe Arg | aaa<br>Lys | 816 |
|                            | 260                |                    | 265                |                    | 270                |                    |            |     |
| caa aat cca<br>Gln Asn Pro | grc ata<br>Xaa Ile | gtt atc<br>Val Ile | gtt caa<br>Val Gln | tac gtg<br>Tyr Val | gat gat<br>Asp Asp | ttg tat<br>Leu Tyr | gta<br>Val | 864 |
|                            | 275                |                    | 280                |                    | 285                |                    |            |     |



```

ggg tct gac tta gaa ata ggg caa cat aga gca aaa ata gag gag ttg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
290                295                300

aga gaa cat ctg ttg agg tgg gga tty ttc aca cca gac gaa aaa cat      960
Arg Glu His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Glu Lys His
305                310                315                320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cac cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                330                335

aaa tgg acc gta cag cct ata aat ttg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Asn Leu Pro Glu Lys Asp Ser Trp Thr
340                345                350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                360                365

att tac tca ggg
Ile Tyr Ser Gly
370

<210> 14
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 14
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                5                10                15

ggg caa gta agg gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Val Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                25                30

tta gaa gaa atg aat ttg cca gga aaa tgg aag cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
35                40                45

gga att ggg ggc ttt atc aaa gta aga cag tat gat caa ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50                55                60

gaa atc tgt gga cat aaa gct ata ggg aca gtg tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
65                70                75                80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
85                90                95

```

|   |      |
|---|------|
| tta aat ttt cct att agt cct att gaa act gtg cca gta aaa tta aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca ttg ata gaa att tgt aca gaa atg gaa aag gaa gga | 432  |
| Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |      |
| 145 150 155 160   |      |
| gcc ata aag aaa aaa aac agt act aga tgg agg aaa cta gta gac ttc | 528  |
| Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat ccc gca gga tta aaa aag aga aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Arg Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gac ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg |      |
| 210 215 220   |      |
| aaa tac act gca ttc acc ata cct agt ata aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly     |      |
| 225 230 235 240   |      |
| att aga tat cag tac aat gtg ctg cca caa gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| tca ata ttc caa agt agy atg aca aaa atc tta gag cct ttt aga aag | 816  |
| Ser Ile Phe Gln Ser Xaa Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac ata gat atc tgt caa tac atg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Ile Asp Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gaa ata ggg cag cat aga gca aaa ata rag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Xaa Glu Leu |      |
| 290 295 300   |      |
| aga gag cat ctg cta aag tgg gga ttt acc aca cca gac raa aaa cat | 960  |
| Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Xaa Lys His |      |
| 305 310 315 320   |      |
| car aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctt cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta caa cat ata gag cta cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln His Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
           355                          360                          365

att tat gca ggg 1116  
 Ile Tyr Ala Gly  
           370

<210> 15  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 15  
 cct caa atc act ctt tgg car cga ccc ctc gtt gca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly  
           1                          5                          10                          15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
                           20                          25                          30

tta kaa gaa atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Xaa Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
           35                          40                          45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta tcc wta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Xaa  
           50                          55                          60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr  
           65                          70                          75                          80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
                           85                          90                          95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                           100                          105                          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
           115                          120                          125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
           130                          135                          140

aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
           145                          150                          155                          160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttg gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175  
 aga gaa ctt aat aag aaa act caa gac ttc tgg gar gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190  
 ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205  
 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg  
 210 215 220  
 aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca gga 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240  
 atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255  
 gca ata ttt caa agy agc atg ata aga aty tta gag cct ttt aga aaa 816  
 Ala Ile Phe Gln Xaa Ser Met Ile Arg Xaa Leu Glu Pro Phe Arg Lys  
 260 265 270  
 caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta 864  
 Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
 275 280 285  
 gga tct gat tta gaa ata gaa cag cat aga gca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ala Lys Ile Glu Glu Leu  
 290 295 300  
 aga caa cat ctg tta agg tgg gga ttt acc aca cca gay aaa aaa cat 960  
 Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320  
 cag aaa gaa cct cca ttc ctt tgg atg gga tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp  
 325 330 335  
 aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350  
 gtc aat gac ata cag aag ttr gtg gga aaa ttr aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Xaa Val Gly Lys Xaa Asn Trp Ala Ser Gln  
 355 360 365  
 att tac tca ggg 1116  
 Ile Tyr Ser Gly  
 370

<210> 16  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)  
 <220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 16
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg caa cta aag gag gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gac atg act ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Thr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
             35             40             45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
             50             55             60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
             65             70             75             80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca tta rta gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
             130            135            140

aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
             145            150            155            160

gcc ata aag aaa aar gat ggt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa att caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly
             180            185            190

ata cca cat cct gca ggg tta aaa aag aaa aag tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
             210            215            220

```

```

aag tat act gca ttt act ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aag      816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gac tta gaa ata ggg cag cat aga rca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Xaa Lys Ile Glu Glu Leu
290                               295                               300

agg caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca caa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Gln Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg
Ile Tyr Pro Gly
370

```

```

<210> 17
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1) ... (297)
<223> HIV Protease

```

```

<221> CDS
<222> (298) ... (1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 17
cct caa atc act ctt tgg caa cga ccc aty gtc aca ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly
1                               5                               10                               15

ggg caa cta aag gaa gcc cta ata gat aca gga gca gat gat aca gtg      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

```

|   |     |
|---|-----|
| tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gct gta ggt tca gtg tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Val Gly Ser Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act<br>Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu<br>115 120 125     | 384 |
| aaa ata gaa gca tta gta gaa atc tgt gca gaa ctg gaa gag gca ggg<br>Lys Ile Glu Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Glu Ala Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Ile Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aar aag aac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aac aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttc tca att ccc tta gat aag gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt aca ata cct agy ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Xaa Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cma cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Xaa Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc cag tgt agc atg aca aaa atc tta gat cct ttt aga aaa<br>Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

gga tct gac tta gaa ata ggg car cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa yat ctg tgg aag tgg gga ttt tac aca cca gag aat aaa cat      960
Arg Gln Xaa Leu Trp Lys Trp Gly Phe Tyr Thr Pro Glu Asn Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc cwt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat gcn ggg
Ile Tyr Ala Gly
370

<210> 18
<211> 1117
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1117)
<223> Portion of HIV Reverse Transcriptase

<400> 18
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg car cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

gta gaa gaa atg aat tta tca gga agg tgg aaa cca aaa atg ata ggg      144
Val Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly
35                               40                               45

gga att gga ggt ttt atc aaa gta aga saa tat gaa cag ata cct gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Xaa Tyr Glu Gln Ile Pro Val
50                               55                               60

gaa att tgt gga cat aaa gct gta ggt aca gta tta gtg gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                               85                               90                               95

```



|   |      |
|---|------|
| tta aat ttt ccc att agt ccc att gaa act gta cca gta aaa ttg aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |      |
| 145 150 155 160   |      |
| gcc ata aag aaa aaa gac agt aat aaa tgg agg aaa tta gtg gat ttc | 528  |
| Ala Ile Lys Lys Lys Asp Ser Asn Lys Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat ccy tca ggg tta aaa aag aaa aaa tca gta aca gta ctg | 624  |
| Ile Pro His Xaa Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tac ttt tca gtt ccc tta gat aaa gaa ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att agr tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca | 768  |
| Ile Xaa Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga gaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Glu |      |
| 260 265 270   |      |
| caa aat aca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta | 864  |
| Gln Asn Thr Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gaa ata ggg cag cat aga gca aaa gtr gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Xaa Glu Glu Leu |      |
| 290 295 300   |      |
| aga caa cat ctg ttg agg tgg gga yta acc aca cca gac aaa aaa cat | 960  |
| Arg Gln His Leu Leu Arg Trp Gly Xaa Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttc cgt tgg atg ggk tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Arg Trp Met Xaa Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gtr caa cct ata gag ctg cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Xaa Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

gtc aat gac ata caa aaa gtt agt ggg aaa att aaa ttg ggc aag tca 1104  
 Val Asn Asp Ile Gln Lys Val Ser Gly Lys Ile Lys Leu Gly Lys Ser  
           355                          360                          365

gat tta ccc agg g 1117  
 Asp Leu Pro Arg  
           370

<210> 19  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 19  
 cct cag atc act ctt tgg caa cga ccc cty gtc aca gta aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Val Lys Ile Gly  
           1                          5                          10                          15

ggg caa cta acg gaa gct yta ttg gat aca gga gca gat aat aca gta 96  
 Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asn Thr Val  
                           20                          25                          30

tta gaa gaa atg agt ttr cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Ser Xaa Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
           35                          40                          45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
           50                          55                          60

gaa atc tgt gga cat aaa gta gta ggt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Val Val Gly Thr Val Leu Ile Gly Pro Thr  
           65                          70                          75                          80

cct gtc aac ata att gga aga gat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr  
                           85                          90                          95

tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                           100                          105                          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
           115                          120                          125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
           130                          135                          140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
           145                          150                          155                          160

|   |      |
|---|------|
| gcc ata aag aaa aar gac agt act aaa tgg aga aaa ttr gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc tca ggg tta aaa aag aaa aaa tca gta aca gta cta<br>Ile Pro His Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gac gtg ggt gat gca tat ttc tca gtt ccc cta gat aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttc acc ata cct agt gta aac aat gag act cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| cac aat cca aac ata gtt atc tat caa tac gtg gat gat tta tat gta<br>His Asn Pro Asn Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg aag tgg ggg ttt tac aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gtg cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata caa aag tta gtg gga aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tac cca ggg<br>Ile Tyr Pro Gly<br>370   | 1116 |

<210> 20  
 <211> 1117  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)  
 <220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1117)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 20
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata gga      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gac ata aat ttg cca ggg aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
             35             40             45

gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata cca gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val
  50             55             60

gaa att tgt gga cat aaa gct gta ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Ile Gly Pro Thr
  65             70             75             80

cct gtc aac gta att gga aga aat ctg atg act cag att ggc tgc act      288
Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggt cca aaa gtt aaa caa tgg cca tta aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca tta gta gaa att tgc aca gaa ttg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
             130            135            140

aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
             145            150            155            160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
             180            185            190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca ata ccc tta gat gaa gaa ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg
             210            215            220

```

```

aag tat act gca ttt acc ata cct agt cca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Pro Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttt caa tgt agt atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

gaa aat cca gat ata gtt atc tac caa tac atg gat gac tta tat gta      864
Glu Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa tat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat      960
Arg Gln Tyr Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag caa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Gln Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag ttt agt ggg aaa att gaa ttg ggc aag tca      1104
Val Asn Asp Ile Gln Lys Phe Ser Gly Lys Ile Glu Leu Gly Lys Ser
355                               360                               365

gat tta tgc agg g
Asp Leu Cys Arg
370

```

```

<210> 21
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

```

```

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 21
cct cag atc act ctt tgg caa cga mcc gtt gtc wca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Xaa Val Val Xaa Ile Lys Ile Gly
1                               5                               10                               15

ggg caa cta aaa gaa gct cta tta gay aca ggg gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

```

|   |     |
|---|-----|
| tta gaa gac atg cat ttg cca ggt aga tgg aaa cca aaa atg ata gtg<br>Leu Glu Asp Met His Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val<br>35 40 45        | 144 |
| gga att ggg ggt ttt gtc aaa gta aga cag tat gat cag ata cct gta<br>Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cca gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act<br>Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttc ccc atc agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa att aga caa tgg cca tta aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Ile Arg Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa aat agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt atg aac aat gag aca cca gga<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Met Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agt atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| cag aat cca gac ata gtc atc tat caa tac atg gat gat tta tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

gga tcg gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ttg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg aga tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                               330                               335

aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                               345                               350

gtt aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt caa      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                               360                               365

att tat gca ggg
Ile Tyr Ala Gly
370

<210> 22
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 22
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag gta gga      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly
1                               5                               10                               15

ggg caa cta aag gag gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

tta gaa gac ata gat ttg cca gga agr tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Ile Asp Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly
35                               40                               45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50                               55                               60

gaa ata tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat ctg ttg act cgg att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Arg Ile Gly Cys Thr
85                               90                               95

```

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |      |
| 145 150 155 160   |      |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt | 528  |
| Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtg caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gay ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg |      |
| 210 215 220   |      |
| aag tat act gcc ttt acc ata cct agt ata aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| ggg tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga gaa cat ctg ttg agg tgg gga ttt acc acc cca gac aaa aaa cat | 960  |
| Arg Glu His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg acc gtr cag cct ata gag ctg cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Xaa Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |



```

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg      1116
Ile Tyr Pro Gly
      370

<210> 23
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 23
cct cag atc act ctt tgg caa cga ccc ata gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
      35                      40                      45

gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile
      50                      55                      60

gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                     105                     110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                     120                     125

aaa ata aaa gca tta aca gaa atc tgt wca gag atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Xaa Glu Met Glu Lys Glu Gly
      130                     135                     140

aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                     150                     155                     160

```

gcy ata cac aag aaa aat agt aat aga tgg aga aaa gta gta gat ttc 528  
Xaa Ile His Lys Lys Asn Ser Asn Arg Trp Arg Lys Val Val Asp Phe  
165 170 175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
180 185 190

ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg 624  
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu  
195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gat ttc agg 672  
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg  
210 215 220

aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg 720  
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
225 230 235 240

atc aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca 768  
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255

gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa 816  
Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys  
260 265 270

caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta 864  
Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val  
275 280 285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata aak gaa ctg 912  
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Xaa Glu Leu  
290 295 300

aga saa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat 960  
Arg Xaa His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His  
305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agt tgg acw 1056  
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Xaa  
340 345 350

gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa 1104  
Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365

att tac cca ggg 1116  
Ile Tyr Pro Gly  
370

&lt;210&gt; 24

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 24
cct cag atc act ctt tgg caa cga ccc ata gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1                               10                               15

ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                20                               25                               30

tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
                35                               40                               45

gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile
                50                               55                               60

gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
                65                               70                               75

cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                85                               90                               95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                100                               105                               110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
                115                               120                               125

aaa ata aaa gca tta aca gaa atc tgt wca gag atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Xaa Glu Met Glu Lys Glu Gly
                130                               135                               140

aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                145                               150                               155

gcy ata cac aag aaa aat agt aat aga tgg aga aaa gta gta gat ttc      528
Xaa Ile His Lys Lys Asn Ser Asn Arg Trp Arg Lys Val Val Asp Phe
                165                               170                               175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                180                               185                               190

ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
                195                               200                               205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gat ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
                210                               215                               220

```

```

aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

atc aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata aak gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Xaa Glu Leu
                               290                               295                               300

aga saa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat      960
Arg Xaa His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agt tgg acw     1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Xaa
                               340                               345                               350

gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa     1104
Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tac cca ggg
Ile Tyr Pro Gly
                               370

```

```

<210> 25
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

```

```

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 25
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg caa cta aag gaa gct cta cta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

```

|   |     |
|---|-----|
| tta gaa gaa atg agt ttg cca gga aaa tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta tcc atg<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Met<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga tct aca<br>Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Ser Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ytg ttg act cag ctt ggg tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Xaa Leu Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gar ggg<br>Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aaa act caa gat ttc tgg gaa rtt caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Xaa Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta caa aag aac aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Gln Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtc ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa tat agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Tyr Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac ata gtt atc tac caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                               330                               335

aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                               360                               365

att tac cca ggg
Ile Tyr Pro Gly
370

<210> 26
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 26
cct cag atc act ctt tgg caa cga ccc atc gtc gaa ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Glu Ile Lys Val Gly
1                               5                               10                               15

ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg      144
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly
35                               40                               45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
50                               55                               60

gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
85                               90                               95

```

|   |      |
|---|------|
| tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aaa | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ytg gaa gag gaa ggg | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Glu Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe |      |
| 145 150 155 160   |      |
| gcc ata aag aag aaa nnn agt ggt aga tgg aga aaa ata gta gat ttt | 528  |
| Ala Ile Lys Lys Lys Xaa Ser Gly Arg Trp Arg Lys Ile Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat ccc gca ggg tta aaa aag aac aag tca gta aca att ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Ile Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gaa ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac ata gtt atc tat cag tac gtg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gat tta gaa ata ggg gag cat aga aca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Glu His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga car cat ctg tta arg tgg gga ttt ttc aca cca gaa caa aaa cat | 960  |
| Arg Gln His Leu Leu Xaa Trp Gly Phe Phe Thr Pro Glu Gln Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct ccm ttc cak tgg atg ggt tat gaa ctc cay cct gat | 1008 |
| Gln Lys Glu Pro Xaa Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta cas cct ata gtg ctg cca gaa aaa gat agc tgg act | 1056 |
| Lys Trp Thr Val Xaa Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
           355                          360                          365

att tac cca ggg 1116  
 Ile Tyr Pro Gly  
           370

<210> 27

<211> 1113

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1)...(297)

<223> HIV Protease

<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

<400> 27

cct cag atc act ctt tgg caa cga ccc atc gtc gaa ata aag gta ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Glu Ile Lys Val Gly  
           1                          5                          10                          15

ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
                           20                          25                          30

tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg 144  
 Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly  
           35                          40                          45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc 192  
 Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile  
           50                          55                          60

gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr  
           65                          70                          75                          80

cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act 288  
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
                           85                          90                          95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aaa 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                           100                          105                          110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu  
           115                          120                          125

aaa ata aaa gca tta gta gaa att tgt aca gaa ytg gaa gag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Glu Glu Gly  
           130                          135                          140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe  
           145                          150                          155                          160



gcc ata aag aag aaa agt ggt aga tgg aga aaa ata gta gat ttt aga 528  
 Ala Ile Lys Lys Lys Ser Gly Arg Trp Arg Lys Ile Val Asp Phe Arg  
 165 170 175

gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga ata 576  
 Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile  
 180 185 190

cca cat ccc gca ggg tta aaa aag aac aag tca gta aca att ctg gat 624  
 Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Ile Leu Asp  
 195 200 205

gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gaa ttc agg aag 672  
 Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg Lys  
 210 215 220

tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg att 720  
 Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile  
 225 230 235 240

aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca gca 768  
 Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala  
 245 250 255

ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa caa 816  
 Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln  
 260 265 270

aat cca gac ata gtt atc tat cag tac gtg gat gat ttg tat gta gga 864  
 Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly  
 275 280 285

tct gat tta gaa ata ggg gag cat aga aca aaa ata gag gaa ctg aga 912  
 Ser Asp Leu Glu Ile Gly Glu His Arg Thr Lys Ile Glu Glu Leu Arg  
 290 295 300

car cat ctg tta arg tgg gga ttt ttc aca cca gaa caa aaa cat cag 960  
 Gln His Leu Leu Xaa Trp Gly Phe Phe Thr Pro Glu Gln Lys His Gln  
 305 310 315 320

aaa gaa cct ccm ttc cak tgg atg ggt tat gaa ctc cay cct gat aaa 1008  
 Lys Glu Pro Xaa Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp Lys  
 325 330 335

tgg aca gta cas cct ata gtg ctg cca gaa aaa gat agc tgg act gtc 1056  
 Trp Thr Val Xaa Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val  
 340 345 350

aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag att 1104  
 Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile  
 355 360 365

tac cca ggg  
 Tyr Pro Gly 1113  
 370

<210> 28  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)  
 <220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 28
cct caa atc act stt tgg caa cga ccc aty gtc tca ata aag ata ggg      48
Pro Gln Ile Thr Xaa Trp Gln Arg Pro Xaa Val Ser Ile Lys Ile Gly
  1                               10                               15

ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
                35                               40                               45

gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
                50                               55                               60

gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca      240
Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr
                65                               70                               75

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                85                               90                               95

tta aat ttt ccc att agt cct atk gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Phe Ile Ser Pro Xaa Glu Thr Val Pro Val Lys Leu Lys
                100                              105                              110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu
                115                              120                              125

aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga      432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly
                130                              135                              140

aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt      480
Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
                145                              150                              155

gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc      528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                165                              170                              175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                180                              185                              190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                195                              200                              205

gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
                210                              215                              220

```

```

aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg ctt gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val
                               275                               280                               285

gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
                               290                               295                               300

aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat      960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gka cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Xaa Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg
Ile Tyr Pro Gly
370

```

```

<210> 29
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 29
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

```

|   |     |
|---|-----|
| tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata<br>Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gtt ata ggt aca gtw tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Val Ile Gly Thr Xaa Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act<br>Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gag gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aag aac agt act agg tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aac aaa tca gca aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Ala Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggc gat gca tat ttt tca gtt ccc tta gac aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acy ata cct agt ata aac aat gaa aca cca ggg<br>Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| tar ata tca gtg tac aat gtr ctt cca caa gga tgg aaa gga tca cma<br>Xaa Ile Ser Val Tyr Asn Xaa Leu Pro Gln Gly Trp Lys Gly Ser Xaa<br>245 250 255     | 768 |
| gca ata ttc maa agt agc atg aca aga atc tta gag cct ttt aga aaa<br>Ala Ile Phe Xaa Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gaa ata gtt atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu
290                295                300

aga caa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His
305                310                315                320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                330                335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                345                350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                360                365

att tac gcg ggg
Ile Tyr Ala Gly
370

<210> 30
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 30
cct caa atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
1                5                10                15

ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
20                25                30

tta gaa gaa atg agc tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35                40                45

gga att gga ggk ttt atc aaa gtg agm cag tat gat cag ata ctc ata      192
Gly Ile Gly Xaa Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Leu Ile
50                55                60

gaa aty tgt gga cat aaa gct ata ggt aca gtr tta ata gga cct aca      240
Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr
65                70                75                80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85                90                95

```

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aaa<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336  |
| cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggr<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa<br>130 135 140     | 432  |
| aaa att aca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aag aaa aac agt gat aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat cca gca ggg tta aaa cag aaa aag tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gta ccc tta gat gaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| gtt aga tat cag tac aat gta ctc cca cag gga tgg aaa gga tca cca<br>Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt agg aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gaa ata gtt atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg agg tgg gga ttc tac aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |

gtc aat gac ata cag aag tta gta ggg aaa tta aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
           355                          360                          365

att tat gca gga 1116  
 Ile Tyr Ala Gly  
           370

<210> 31  
 <211> 1117  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 31  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
           1                          5                          10                          15

ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
                           20                          25                          30

cta gaa gac gtg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Asp Val His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
           35                          40                          45

gga att gga ggt ttt atc aaa gta aga cag tat gat gag gta ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Glu Val Pro Ile  
           50                          55                          60

gaa ctc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240  
 Glu Leu Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
           65                          70                          75                          80

ccc gtc aac ata att gga aga aat ctg wtg act caa ctt ggg tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Leu Gly Cys Thr  
                           85                          90                          95

cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                           100                          105                          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
           115                          120                          125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
           130                          135                          140

aaa att tca aga gtt ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Arg Val Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
           145                          150                          155                          160

|   |      |
|---|------|
| gyc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cay ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc aga<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gat cct ttt agg aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aac cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tcy gac tta gaa ata gga cag cat agr rca aaa ata gaa gaa ctg<br>Gly Xaa Asp Leu Glu Ile Gln His Xaa Xaa Lys Ile Glu Glu Leu<br>290 295 300         | 912  |
| aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aag aaa cat<br>Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| car aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gtg cag cct ata gtg ctg cca gaa aag gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ant aca gaa gtt agt ggg aaa att gaa ttg ggc aag tca<br>Val Asn Asp Xaa Thr Glu Val Ser Gly Lys Ile Glu Leu Gly Lys Ser<br>355 360 365     | 1104 |
| gat tta tgc agg g<br>Asp Leu Cys Arg<br>370   | 1117 |

<210> 32  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)  
 <220>



<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 32
cct caa atc act ctt tgg caa cga ccc cty gtc gca ata agg ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Ala Ile Arg Ile Gly
1          5          10          15

ggg caa cta aag gaa gcc cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20          25          30

tta gaa gac atg gag ttg cca gga aga tgg aag cca aaa atg ata ggg      144
Leu Glu Asp Met Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35          40          45

gga att gga ggt ttt atc aaa gta aam cag tat gat cag ata ctt gta      192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Leu Val
          50          55          60

gaa atc tgt gga cat aaa gct gta ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Ile Gly Pro Thr
65          70          75          80

cct gtc aac ata att gga aga aat ttg ttg act cag att ggc tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
          85          90          95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Phe Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
          115          120          125

aaa ata aaa gca tta gta gaa atc tgt aca gaa ttg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
          130          135          140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145          150          155          160

gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
          165          170          175

aga gaa ctt aat aaa aga act caa gac ttt tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
          180          185          190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tcc gtg aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
          195          200          205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttt aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
210          215          220

```

aag tat act gca ttt acc aya cct sgt ata aac aat gag aca cca ggg 720  
Lys Tyr Thr Ala Phe Thr Xaa Pro Xaa Ile Asn Asn Glu Thr Pro Gly  
225 230 235 240  
  
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcc cca 768  
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255  
  
gca ata ttt caa agc agc atg aca aaa atc tta gag cct ttt aga aaa 816  
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
260 265 270  
  
caa aat cca gac wta gtt wtc tat caa twc ata gat gat ctg tat gta 864  
Gln Asn Pro Asp Xaa Val Xaa Tyr Gln Xaa Ile Asp Asp Leu Tyr Val  
275 280 285  
  
ggc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912  
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu  
290 295 300  
  
aga cag cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat 960  
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His  
305 310 315 320  
  
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335  
  
aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act 1056  
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350  
  
gtc aat gac ata cag aar tta gtg gga aaa ttg aat tgg gca agt cag 1104  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365  
  
att tac cca ggg 1116  
Ile Tyr Pro Gly  
370

<210> 33  
<211> 1116  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease  
  
<221> CDS  
<222> (298)...(1116)  
<223> Portion of HIV Reverse Transcriptase

<400> 33  
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48  
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
1 5 10 15  
  
ggg caa cta aag gaa gct cta tta kat aca gga gca gat gat aca gtm 96  
Gly Gln Leu Lys Glu Ala Leu Leu Xaa Thr Gly Ala Asp Asp Thr Xaa  
20 25 30

|   |     |
|---|-----|
| tta gaa gac atg act ttg cca gga aga tgg aaa cca aaa atg ata ggg<br>Leu Glu Asp Met Thr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aaa cag tat gag gag ata ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Glu Ile Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca ttw gta gaa att tgt gca gaa ctg gaa aag gaa ggg<br>Lys Ile Lys Ala Xaa Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac ggt act aaa tgg aga aag gta aca gat ttt<br>Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Val Thr Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag agg ach caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Xaa Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc tca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aac aat gcg aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Ala Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu  
 290 295 300

aga caa cat ctg ttg aag tgg ggt ttt acc aca cca gac aaa aaa cat 960  
 Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tat tca ggg 1116  
 Ile Tyr Ser Gly  
 370

<210> 34  
 <211> 1119  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1119)  
 <223> Portion of HIV Reverse Transcriptase

<400> 34  
 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly  
 1 5 10 15

ggg cag cta aag gaa gct cta ttr gac aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Xaa Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly  
 35 40 45

gga att gga ggt ttt att aaa gta aaa cag tat gaa cag ata acc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Thr Ile  
 50 55 60

gam atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca 240  
 Xaa Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac gta att gga aga aat atg atg act cag att ggt tgc act 288  
 Pro Val Asn Val Ile Gly Arg Asn Met Met Thr Gln Ile Gly Cys Thr  
 85 90 95

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336  |
| cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aac aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta cca aag aac aaa tca gta acg gta ctg<br>Ile Pro His Pro Ala Gly Leu Pro Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672  |
| aag tac act gca ttt acc ata cct agg tat aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Arg Tyr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| act aga tat cag tac aat gtg ctt cct atg gga tgg aaa gga tca cca<br>Thr Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aga<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Arg<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tac gtg gat gac ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gag ata ggg cag cat aga gcg aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga gaa cat ctg tgg aag tgg ggt ttt tac aca cca gac aaa aaa cat<br>Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |

gtc aat gac ata cag aaa tta gtg ggr aaa att gaa ttt ggg cga gtc 1104  
 Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Ile Glu Phe Gly Arg Val  
 355 360 365

aga ttt amc caa ggg 1119  
 Arg Phe Xaa Gln Gly  
 370

<210> 35  
 <211> 1115  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1115)  
 <223> Portion of HIV Reverse Transcriptase

<400> 35

cct cag atc act ctt tgg caa cga ccc cty gtc cca ata arg ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Pro Ile Xaa Ile Gly  
 1 5 10 15

ggg caa tta aag gaa gct cta cta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
 20 25 30

tta gaa gac atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aar gta aaa cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60

gaa atc tgt ggg cat aaa gct ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr  
 85 90 95

cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

|   |      |
|---|------|
| gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtc caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta tta<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg gga gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aag<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtc ata tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| ggg tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cac ttg ttg maa tgg gga ttc acc aca cca gac aaa aag cat<br>Arg Gln His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata kaa ctg cca gaa aaa gac agc tgg ctg<br>Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Leu<br>340 345 350     | 1056 |
| tca atg aca tac aga aat tag tgg gaa agt tga att ggg caa gtc aaa<br>Ser Met Thr Tyr Arg Asn * Trp Glu Ser * Ile Gly Gln Val Lys<br>355 360 365         | 1104 |
| ttt atg cng gg<br>Phe Met Xaa   | 1115 |

&lt;210&gt; 36

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 36
cct cag atc act ctt tgg caa cga cca gtc gtc aca ata aag gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Ile Lys Val Gly
1          5          10

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20          25          30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35          40          45

gga att gga ggt ttt rtc aaa gta aga cag tat gat caa ata ccc ata      192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
          50          55          60

gaa atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr
65          70          75          80

cct gyc aac ata att gga aga aat ctg ttg act cag att ggg tgc act      288
Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
          85          90          95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ctg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
          115          120          125

aaa ata aaa gca tta gta gaa att tgt gca gaa ttg gaa aag gaa ggg      432
Lys Ile Lys Lys Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly
130          135          140          145

aag att tca aaa att ggg ccy gaa aat cca tac aay act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Xaa Glu Asn Pro Tyr Asn Thr Pro Val Phe
145          150          155          160

gcc ata aag aaa aar aac agt act ara tgg aga aaa kta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Ser Thr Xaa Trp Arg Lys Xaa Val Asp Phe
          165          170          175          180

aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
          180          185          190          195

ata cca cat ccc gca ggg cta aag aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
          195          200          205          210

gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat gaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
210          215          220          225

```



|   |      |
|---|------|
| aag tat aca gcc ttt acc tat act ggt tcc aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Tyr Thr Gly Ser Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agc agc atg aca aaa gtc tta gaa cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Val Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg tta agg tgg gga ttt tac aca cca gac gaa aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Glu Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtt aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gcc agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tac cca ggg<br>Ile Tyr Pro Gly<br>370   | 1116 |

<210> 37  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|   |    |
|---|----|
| <400> 37<br>cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aaa ata ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly<br>1 5 10 15 | 48 |
| ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta<br>Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val<br>20 25 30              | 96 |

|   |     |
|---|-----|
| tta gaa gac atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg<br>Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ctg atg aca cag ctt ggt tgt act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| agg gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta ggg<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat cct gca gga tta aaa aag aat aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa att tta gat cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys<br>260 265 270     | 816 |
| cag aat cca gat ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

gga tct gac tta gag ata ggg cag cat aga gca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu  
 290 295 300

aga gca cat ctg ttg aag tgg gga ttt acc acc cca gac aaa aaa cat 960  
 Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tac gca ggg 1116  
 Ile Tyr Ala Gly  
 370

<210> 38  
 <211> 1117  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1117)  
 <223> Portion of HIV Reverse Transcriptase

<400> 38  
 cct caa tca ctt ctt tgg caa cga ccc mtc gtc aca ata aag gta ggg 48  
 Pro Gln Ser Leu Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly  
 1 5 10 15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca ata 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile  
 20 25 30

tta gaa gac aya rat ttg cca ggg aga tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Asp Xaa Xaa Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly  
 35 40 45

gga att gga ggt ttt atc aga gta aga cag tat gat cag gta ccc ata 192  
 Gly Ile Gly Gly Phe Ile Arg Val Arg Gln Tyr Asp Gln Val Pro Ile  
 50 55 60

gaa atc tgt gga cat aaa gtt gta agt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Val Val Ser Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act 288  
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
 85 90 95

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt gaa gaa ttg gaa aag gat ggg | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Glu Glu Leu Glu Lys Asp Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |      |
| 145 150 155 160   |      |
| gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc | 528  |
| Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu     |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gac ttc aga | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Asp Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| tca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa | 816  |
| Ser Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac ata gtc atc tat caa tat atg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gag ata ggg cag cat aga aca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga cag cat ctg tgg aag tgg ggg ttt tac aca cca gac ara aaa cat | 960  |
| Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Xaa Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
                   355                                  360                                  365

att tan tsc agg g 1117  
 Ile Xaa Xaa Arg  
                   370

<210> 39  
 <211> 1128  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1128)  
 <223> Portion of HIV Reverse Transcriptase

<400> 39  
 cct cag atc act ctt tgg caa cga cca ttc gtc aca ata aaa ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Ile Lys Ile Gly  
           1                                  5                                  10                                  15

ggg caa cta aag gaa gct ata tta gac aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Thr Val  
                   20                                  25                                  30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
                   35                                  40                                  45

gga att gga ggt ttt mtc aaa gta aga cag tat gat cag gta ccc ata 192  
 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Val Pro Ile  
           50                                  55                                  60

gaa atc tgt gga cat aaa gtt atg agt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Val Met Ser Thr Val Leu Ile Gly Pro Thr  
           65                                  70                                  75                                  80

cct gtc aac ata att gga aga aat ctg atg act cag mtt ggc tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Xaa Gly Cys Thr  
                   85                                  90                                  95

tta aat ttt ccc att agt cct att gaa act gwa cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Xaa Pro Val Lys Leu Lys  
                   100                                  105                                  110

cca ggg atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
                   115                                  120                                  125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
           130                                  135                                  140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
           145                                  150                                  155                                  160

|   |      |
|---|------|
| gcc ata aag aaa aaa gac agt aat aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Asn Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtc caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gat tca gra<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp Ser Xaa<br>210 215 220     | 672  |
| agt aca ctg cat tta cca tac cta gta cgr acc aat gag aca cca ggg<br>Ser Thr Leu His Leu Pro Tyr Leu Val Xaa Thr Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac tta gtt atc tgt caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gat tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat<br>Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta caa gcc tat aaa gct gcc aga aaa aga cag ctg gac<br>Lys Trp Thr Val Gln Ala Tyr Lys Ala Ala Arg Lys Arg Gln Leu Asp<br>340 345 350     | 1056 |
| tgt caa tga cat tac mag aaa gtt agt ggg gaa aat tgg aat ttg ggg<br>Cys Gln * His Tyr Xaa Lys Val Ser Gly Glu Asn Trp Asn Leu Gly<br>355 360 365       | 1104 |
| caa ggt cag att tat tgc cag ggg<br>Gln Gly Gln Ile Tyr Cys Gln Gly<br>370 375   | 1128 |

<210> 40  
 <211> 1120  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1120)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 40
cct cag atc act ctt tgg caa cga ccc ctc gtt gca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly
  1                      5                      10                      15

gga cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gaa atg agt ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ccm rta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Xaa
                      50                      55                      60

gaa att tgc gga cat aaa gct gta ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
                      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                      145                      150                      155                      160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                      165                      170                      175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                      180                      185                      190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                      195                      200                      205

gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agr      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Xaa
                      210                      215                      220

```

aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg 720  
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly  
225 230 235 240  
  
att aga tat cag tcc aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
Ile Arg Tyr Gln Ser Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255  
  
gca ata ttc caa agt agc atg aca aaa atc cta gaa cct ttt agg aaa 816  
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
260 265 270  
  
caa aat cca gat ata gtt atc tat caa tac atg gat gat cta tat gta 864  
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
275 280 285  
  
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg 912  
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu  
290 295 300  
  
aga caa cat ctg ttg agg tgg ggg ttt acc acc cca gac aaa aaa cat 960  
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
305 310 315 320  
  
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335  
  
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350  
  
gtc aat gac nat aca aaa gtt agt ggg gaa aat tga att ggg sca agt 1104  
Val Asn Asp Xaa Thr Lys Val Ser Gly Glu Asn \* Ile Gly Xaa Ser  
355 360 365  
  
cag att tat tgg agg g 1120  
Gln Ile Tyr Trp Arg  
370

<210> 41  
<211> 1059  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease

<221> CDS  
<222> (298)...(1059)  
<223> Portion of HIV Reverse Transcriptase

<400> 41  
cct caa atc act ctt tgg cag cga ccc gtt gtc aca ata aac ata ggg 48  
Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Ile Asn Ile Gly  
1 5 10 15  
  
ggg caa cta aag gaa gct cta tta gac aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30



|   |     |
|---|-----|
| tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca<br>Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aac ccg tac aat act cca gtc ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gat agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aac aag aaa act caa gac ttc tgg gaa att caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624 |
| gat gtg ggt gat gca tat ttc tca gtt cct tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt aca aac aat gag acg cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gcc ata nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn<br>Ala Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa<br>260 265 270         | 816 |
| nnn nnn nnn nnn nnn nnn nnn tat caa tac atg gat gat ttg tat gta<br>Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag aaa ctg 912  
 Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Lys Leu  
 290 295 300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gat aaa aaa cat 960  
 Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc 1059  
 Val

<210> 42  
 <211> 1053  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1053)  
 <223> Portion of HIV Reverse Transcriptase

<400> 42  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata arg ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Xaa Ile Gly  
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atm aaa gta aga cag tat gat cag ata cyc ata 192  
 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile  
 50 55 60

gaa atc tgt gga yat aaa gct ata ggt acr gta tta gta gga ccc acg 240  
 Glu Ile Cys Gly Xaa Lys Ala Ile Gly Xaa Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac rta att gga aga aat ctg wtg act cag att ggt tgc act 288  
 Pro Val Asn Xaa Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

|   |      |
|---|------|
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttr gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtc caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca kgg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Xaa<br>225 230 235 240 | 720  |
| att aga tay cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata tty caa tgt agc atg aca aaa atc tta gag cct ttt aga aag<br>Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac cta gtt att tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg ara tgg gga ttt acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg gca gtg caa cct ata gtg ctg cca gaa aaa gac agc tgg<br>Lys Trp Ala Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp<br>340 345 350             | 1053 |

<210> 43  
<211> 1082

<212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1082)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 43
cct caa atc act ctt tgg caa cga ccc ctt gtc aca rta aag rta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Xaa Lys Xaa Gly
   1               5               10               15

ggg caa cta aag gaa gct yta ttr gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Xaa Xaa Asp Thr Gly Ala Asp Asp Thr Val
               20               25               30

tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
               35               40               45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
               50               55               60

gaa aty tgt ggg cat aaa gct ata ggt aca gta tta gta ggg cct aca      240
Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
               65               70               75

cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
               85               90               95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
               100              105              110

cca gga atg gat ggc ccc aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
               115              120              125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
               130              135              140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
               145              150              155

gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
               165              170              175

aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
               180              185              190

ata ccg cat ccc gca ggg tta aaa aag aaa aag tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
               195              200              205

```

|   |      |
|---|------|
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aaa tat ast gca ttt acc ata ccg agt ata aac aat gag aca cca ggg<br>Lys Tyr Xaa Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt ccg cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa tgt agc atg aca aaa atc tta gaa cct ttt aga aaa<br>Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac ttg gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga cag cat ctg ttg aaa tgg ggr ttt acc aca cca gac aag aaa cat<br>Arg Gln His Leu Leu Lys Trp Xaa Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta caa ccg ata gag ctg cca gaa aaa gaa agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Glu Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gg<br>Val Asn Asp Ile Gln Lys Leu Val<br>355 360  | 1082 |

<210> 44  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|   |    |
|---|----|
| <400> 44<br>cct cag atc act ctt tgg caa cga ccc atc gtc aca gta aag ata ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Gly<br>1 5 10 15 | 48 |
| ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta<br>Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val<br>20 25 30              | 96 |

|  |     |
|--|-----|
| tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa ata ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly | 144 |
| 35<br>40<br>45   |     |
| gga att gga ggt ttt gcc aaa gta aga cag tat gat cag ata ccc ata<br>Gly Ile Gly Gly Phe Ala Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile | 192 |
| 50<br>55<br>60   |     |
| gaa atc tka gga cat aaa gtt ata ggt aca gtc tta gta gga cct aca<br>Glu Ile Xaa Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr | 240 |
| 65<br>70<br>75<br>80   |     |
| cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act<br>Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr | 288 |
| 85<br>90<br>95   |     |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys | 336 |
| 100<br>105<br>110  |     |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu | 384 |
| 115<br>120<br>125  |     |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly | 432 |
| 130<br>135<br>140  |     |
| aaa att tca aag att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe | 480 |
| 145<br>150<br>155<br>160   |     |
| gcc ata aag aaa aaa aac agy act wga tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Xaa Thr Xaa Trp Arg Lys Leu Val Asp Phe | 528 |
| 165<br>170<br>175  |     |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa ttr gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Xaa Gly | 576 |
| 180<br>185<br>190  |     |
| ata cca cat ccc tca ggg tta aaa aag aam aaa tca gta aca gta ctg<br>Ile Pro His Pro Ser Gly Leu Lys Lys Xaa Lys Ser Val Thr Val Leu | 624 |
| 195<br>200<br>205  |     |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg | 672 |
| 210<br>215<br>220  |     |
| aaa tat act gca ttt acc ata cct agt rta aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Thr Pro Gly | 720 |
| 225<br>230<br>235<br>240   |     |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro | 768 |
| 245<br>250<br>255  |     |
| gca ata ttc caa agt agc atg aca aga atc cta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys | 816 |
| 260<br>265<br>270  |     |
| cag aat cca gac ata gtt atc tat caa tac gtg gat gac ttg ctt gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val | 864 |
| 275<br>280<br>285  |     |

```

gga tct gat tta gaa ata ggg caa cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
   290                               295                               300

aga caa cat ctg ttg agg tgg ggg ttt atc aca cca gac gaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Ile Thr Pro Asp Glu Lys His
   305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                   325                               330                               335

aaa tgg aca gta cag ccc ata gtg ctg cca gaa aaa gay agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                   340                               345                               350

gtc aat gac ata caa aag tta gtg gga aaa ttg aat tgg gca agc cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                   355                               360                               365

att tat gca ggg
Ile Tyr Ala Gly
   370

<210> 45
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 45
cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
   1                               5                               10                               15

ggg cag cta aag gaa gct cta tta gat aca gga gca gac gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                   20                               25                               30

tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa atg ata gtg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Val
                   35                               40                               45

gga att gga gga ttt gtc aaa gta aaa cag tat gag caa ata cct gta      192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Glu Gln Ile Pro Val
                   50                               55                               60

gaa atc tgt gga cat aaa gct gta ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
   65                               70                               75                               80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                   85                               90                               95

```

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gar | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu |      |
| 115 120 125   |      |
| aaa ata maa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga | 432  |
| Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |      |
| 145 150 155 160   |      |
| gct ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc | 528  |
| Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag agg act caa gac ttc tgg gaa att caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat ccc gca ggg tta aaa aag aag aaa tca gta aca rta cta | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Xaa Leu     |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca rtt ccc tta gat aaa gaa ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Xaa Pro Leu Asp Lys Glu Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa gct agc atg aca aaa atc tta gag cct ttc aga aaa | 816  |
| Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gaa cta gtt atc tat caa tac gtg gat gac ttg tat gta | 864  |
| Gln Asn Pro Glu Leu Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga gaa cat ctg tta aaa tgg gga tta ttc aca cca gac cag aaa cat | 960  |
| Arg Glu His Leu Leu Lys Trp Gly Leu Phe Thr Pro Asp Gln Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa ccc cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg act ata cag cct atg gtg ctg cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Ile Gln Pro Met Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |



```

gtc aat gac cta cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Leu Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat cca ggg      1116
Ile Tyr Pro Gly
      370

<210> 46
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 46
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile
      50                      55                      60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gac ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gag att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

```

gcc ata aag aaa aaa gac agt act aag tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aaa aga act caa gac ttc tgg gag gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggc gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg  
 210 215 220

aaa tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240

act aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca 768  
 Thr Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255

gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa 816  
 Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
 260 265 270

caa aat cca gac cta gtt atc tat caa tac atg gat gat ttg tat gta 864  
 Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
 275 280 285

gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Gln His Arg Thr Lys Ile Glu Glu Leu  
 290 295 300

aga caa cat ctg ttg agg tgg gga ttt acc acc cca gac aaa aaa cat 960  
 Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gtr cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Xaa Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tac cca ggg 1116  
 Ile Tyr Pro Gly  
 370

<210> 47  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 47
cct caa atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
  1               5               10               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
              20               25               30

tta gaa gac atg tgt ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
              35               40               45

gga att gga ggt ttt atc aaa gta aga caa tat gat cag gta gcc atg      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ala Met
  50               55               60

gaa atc tgt gga cat aag gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
  65               70               75               80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Thr Gln Ile Gly Cys Thr
              85               90               95

tta aat ttt ccc att agc cct att gaa act gta ccm gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Xaa Val Lys Leu Lys
              100              105              110

cca ggr atg gat ggt cca agg gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Xaa Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
              115              120              125

aaa ata ara gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
              130              135              140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
              145              150              155              160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
              165              170              175

aga gaa ctt aat aag aaa act caa gac tty tgg gaa gtt caa tta ggr      576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Xaa
              180              185              190

ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctt      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
              195              200              205

gat gtg gga gat gca tat ttt tca gtt ccc tta gat aaa gat ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
              210              215              220

```

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720  
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
225 230 235 240  
  
att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255  
  
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aag 816  
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
260 265 270  
  
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta 864  
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val  
275 280 285  
  
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctr 912  
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa  
290 295 300  
  
aga caa cat ctg ttg aag tgg ggg ytt acc aca cca gac aag aaa cat 960  
Arg Gln His Leu Leu Lys Trp Gly Xaa Thr Thr Pro Asp Lys Lys His  
305 310 315 320  
  
cag aaa gaa ccy cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat 1008  
Gln Lys Glu Xaa Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp  
325 330 335  
  
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350  
  
gtc aat gac ata cag aag tta gtg gga aar ttg aat tgg gca agt cag 1104  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365  
  
att tat gca ggg 1116  
Ile Tyr Ala Gly  
370

<210> 48  
<211> 1115  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease

<221> CDS  
<222> (298)...(1115)  
<223> Portion of HIV Reverse Transcriptase

<400> 48  
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg 48  
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly  
1 5 10 15  
  
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30

|   |     |
|---|-----|
| ata gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg<br>Ile Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aaa cag tat gag cag gta ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Val Pro Ile<br>50 55 60        | 192 |
| gaa ctc tgt ggg cgt aaa act ata ggt aca gta tta gta gga cct aca<br>Glu Leu Cys Gly Arg Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aac ctg atg act cag att ggt tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcy ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat cct gca ggg tta aaa aag aag aaa tca gta aca gta ttg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccg tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctk cca cag gga tgg aag gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Xaa Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc ttg gag ccc ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac cta gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

ggc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg aag tgg gga ttt acc aca cca gat aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                               360                               365

att tcc car ga      1115
Ile Ser Gln
370

<210> 49
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 49
cct cag atc act ctt tgg caa cga ccc ctc gtc rca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Xaa Ile Lys Ile Gly
1                               5                               10                               15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aag atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35                               40                               45

gga att gga ggt ttc atc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50                               55                               60

gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat cta ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85                               90                               95

```

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aag tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336  |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile ggg Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175         | 528  |
| aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat cct gca ggg tta aaa aag aam aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Ser Val Thr Val Leu<br>195 200 205         | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672  |
| aag tat acc gca ttt cca tcc cta gtt ata aac aat gag aca cca gga<br>Lys Tyr Thr Ala Phe Pro Ser Leu Val Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gag ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |

```

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agc cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg      1116
Ile Tyr Pro Gly
      370

<210> 50
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 50
cct cag atc act ctt tgg caa cga ccc ttc gtc aac ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Asn Ile Lys Ile Gly
      1                      5                      10                      15

gga caa ctg aag gaa gct cta ttg gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
      35                      40                      45

gga att gga ggt ttk gtc aaa gta aga cag tat gat cag ata cct gta      192
Gly Ile Gly Gly Xaa Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val
      50                      55                      60

gaa att tgt gga cat aaa gyt ata ggt aca gtc tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Xaa Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
      130                      135                      140

aaa att tca aag att ggg cct gaa aat cca tac aat act cca ata ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
      145                      150                      155                      160

```



```

gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                                165                                170                                175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                                180                                185                                190

ata cca cat ccc gca ggg tta mam aag aac aaa tca gta aca gtg cta      624
Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu
                                195                                200                                205

gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg
                                210                                215                                220

aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
                                225                                230                                235                                240

att aga tat cag tay aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                                245                                250                                255

gca ata ttc cag agt agc atg aca aga atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys
                                260                                265                                270

caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta      864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
                                275                                280                                285

gca tct gac tta gaa ata gag aaa cat aga aca aaa ata gag gaa ctg      912
Ala Ser Asp Leu Glu Ile Glu Lys His Arg Thr Lys Ile Glu Glu Leu
                                290                                295                                300

aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aag cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
                                305                                310                                315                                320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                                325                                330                                335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                                340                                345                                350

gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                                355                                360                                365

att tat gga ggg
Ile Tyr Gly Gly
                                370

```

```

<210> 51
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>

```

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 51
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
             35             40             45

gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata cct ata      192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
             50             55             60

gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr
             65             70             75

cct gcc aac ata att gga aga gat ctg ttg act cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
             130            135            140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cct gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
             145            150            155

gcc ata aag aaa aaa aac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
             180            185            190

ata cca cat ccc gcg ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg
             210            215            220

```

|   |      |
|---|------|
| aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| gtt aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag ccc ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tat gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg tgg agg tgg ggg ttt tac aca cca gac aaa aaa cat<br>Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta caa cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aaa tta gtg ggg aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |

<210> 52  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|   |    |
|---|----|
| <400> 52<br>cct caa atc act ctt tgg caa cga ccc ctt gtc aca ata aag rta ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Xaa Gly<br>1 5 10 15 | 48 |
| ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta<br>Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val<br>20 25 30              | 96 |

|   |     |
|---|-----|
| tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atr ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ycc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gct ata ggt tca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata aty gga aga aat ctg atg act cag att ggt tgc act<br>Pro Val Asn Ile Xaa Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa ack gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Xaa Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gra gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Xaa Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aga att ggg ccc gaa aat cca tac aat act cca ata ttt<br>Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aag aat agt act aga tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aac aaa tca gtg aca gta ytg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Xaa<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt atr aac aat gag aaa cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Lys Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca car gga tgg aaa ggg tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa tgt agc atg aca aaa aty tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Cys Ser Met Thr Lys Xaa Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| car aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ttg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
  290                      295                      300

aga caa cat ctg tta agg tgg gga ttt ttc aca cca gaa caa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His
  305                      310                      315                      320

cag aaa gaa ccg cca ttc ctt tgg atg ggt tat gaa cta cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg acg gta cag cct ata aag ctg cca gaa aaa gat agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tay gca ggg
Ile Tyr Ala Gly
  370
      1116

<210> 53
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 53
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1                      5                      10                      15

ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gtg aga cag tat gat cag rta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile
                      50                      55                      60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga tct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr
                      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                      85                      90                      95

```

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |      |
| 145 150 155 160   |      |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc | 528  |
| Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| atc cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc cgg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca gga | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt agg aat | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Asn |      |
| 260 265 270   |      |
| aaa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta | 864  |
| Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac cta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga gaa cat ctg ttg aag tgg ggg ttt act aca cca gac aaa aaa cat | 960  |
| Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gtc cag cct ata gag ctg cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

```

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat gca gga
Ile Tyr Ala Gly
      370

<210> 54
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 54
cct cag atc act ctt tgg caa cga ccc aty gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata gtg      144
Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
      35                      40                      45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
      50                      55                      60

gaa atc tgt gga cat aaa att ata ggt aca gta tta ata gga aat aca      240
Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Asn Thr
      65                      70                      75                      80

cct gcc aac gta att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Ala Asn Val Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

```

|   |      |
|---|------|
| gcc ata aag aaa aag gac agt act aaa tgg aga aaa gta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aac aag aga act caa gac ttc tgg gag gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cac ccc gca ggg ata aaa aag aat aaa tca gta act gta cta<br>Ile Pro His Pro Ala Gly Ile Lys Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gta ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672  |
| aaa tat act gca ttc acc ata cct agt att aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cac aga ata aaa ata rag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Xaa Glu Leu<br>290 295 300     | 912  |
| aga gaa cat cta tgg aag tgg gga ttt tac aca cca gac aaa aag cat<br>Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata acg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg ggg aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |

&lt;210&gt; 55

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;



<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 55  
 cct caa atc act ctt tgg caa cga ccc ctc gtc gca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly  
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gtc 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aag cag tat gat cag gta ctt gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Leu Val  
 50 55 60

gaa att tgt gga cat ara gct ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Xaa Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgt act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca ggt atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcc ata aag aaa aaa gac agt acc aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aaa acg caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg  
 210 215 220

|   |      |
|---|------|
| aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata gag cag cat aga rca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Xaa Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| agg cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata ktg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tam ccc ngg<br>Ile Xaa Pro Xaa<br>370   | 1116 |

<210> 56  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|   |    |
|---|----|
| <400> 56<br>cct caa atc act ctt tgg caa cga ccc att gtc aca ata aag ata ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly<br>1 5 10 15 | 48 |
| ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta<br>Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val<br>20 25 30              | 96 |

|  |     |
|--|-----|
| tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata acc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Thr Ile | 192 |
| gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr | 240 |
| cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe | 480 |
| gcc ata aag aaa aaa gat agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe | 528 |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gta caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg | 672 |
| aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro | 768 |
| gca ata ttc caa agc agc atg aca aaa att tta gaa cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys | 816 |
| caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val | 864 |

```

gga tct gac tta raa ata gag cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Xaa Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa cag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Gln Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg
Ile Tyr Pro Gly
370

<210> 57
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 57
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag tta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Leu Gly
1                               5                               10                               15

ggg caa cta atg gaa gtt cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Met Glu Val Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

rta gaa gaa ata agt tta cca gga aga tgg aaa cca aaa atg ata ggg      144
Xaa Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                               35                               40                               45

gga att gga ggt ttt gtc aaa gta aaa cag tat gat cag gta ccc tta      192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Val Pro Leu
50                               55                               60

gaa att tgt gga aaa aag gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly Lys Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65                               70                               75                               80

cct gcc aac ata att gga aga aat ttt ttg gct cag att ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Phe Leu Ala Gln Ile Gly Cys Thr
                               85                               90                               95

```

|   |      |
|---|------|
| tta aat ttc ccc att agt cct att gaa act gta cca gta aaa tta aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480  |
| Lys Ile Ser Lys Ile ggg cct gaa aat cca tac aat act cca gta ttt |      |
| 145 150 155 160   |      |
| gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttt | 528  |
| Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag agg acs caa gac ttc tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Xaa Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat ccc gca ggg tta aar aag aac aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cca ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac caa aaa cat | 960  |
| Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Gln Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta cag cct ata acg ctg cca gac aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Asp Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

```

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat gca ggg      1116
Ile Tyr Ala Gly
      370

<210> 58
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 58
cct caa atc act ctt tgg caa cga ccc cta gtt aca ata aaa ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ctc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
      50                      55                      60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag atc ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aga gtt aar caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

```

```

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                                165                                170                                175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                                180                                185                                190

ata cca cat cca gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                                195                                200                                205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
                                210                                215                                220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
                                225                                230                                235                                240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                                245                                250                                255

gca ata ttc caa agt agc atg aca ata atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Ile Ile Leu Glu Pro Phe Arg Lys
                                260                                265                                270

caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                                275                                280                                285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                                290                                295                                300

aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
                                305                                310                                315                                320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat     1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                                325                                330                                335

aaa tgg aca gta cag cct ata aag ctg cca gac aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asp Lys Asp Ser Trp Thr
                                340                                345                                350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                                355                                360                                365

att tat gca gga
Ile Tyr Ala Gly
                                370

```

```

<210> 59
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
<220>

```

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 59  
 cct caa atc act ctt tgg caa cga ccc tta gtc aca ata aag ata grg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Xaa  
 1 5 10 15

ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa ata aat ttg cca ggg aaa tgg aaa cca maa atg ata ggg 144  
 Leu Glu Glu Ile Asn Leu Pro Gly Lys Trp Lys Pro Xaa Met Ile Gly  
 35 40 45

gga att gga ggt ttt att aaa gta aga cag tat gat caa ata gcc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile  
 50 55 60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta rta gaa atc tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcm ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttc tca gtt ccc tta gac caa gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg  
 210 215 220



aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720  
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
225 230 235 240  
  
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255  
  
gca ata ttc caa agt agc atg aca agg atc tta gar cct ttt aga aaa 816  
Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys  
260 265 270  
  
caa aat cca gaa ata gtc aty tat cag tac atg gat gat tta tat gta 864  
Gln Asn Pro Glu Ile Val Xaa Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
275 280 285  
  
gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg 912  
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu  
290 295 300  
  
aga caa cat ctg ttg agr tgg ggg ttt tmc acg cca gac aaa aag cat 960  
Arg Gln His Leu Leu Xaa Trp Gly Phe Xaa Thr Pro Asp Lys Lys His  
305 310 315 320  
  
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335  
  
aaa tgg aca gta cag act ata gaa ctg cca gaa aaa gat agc tgg act 1056  
Lys Trp Thr Val Gln Thr Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350  
  
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365  
  
ata tac cca ggg 1116  
Ile Tyr Pro Gly  
370

<210> 60  
<211> 1116  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease

<221> CDS  
<222> (298)...(1116)  
<223> Portion of HIV Reverse Transcriptase

<400> 60  
cct caa atc act ctt tgg cag cga ccc cty gtc aca ata aag ata ggg 48  
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly  
1 5 10 15  
  
ggg caa cta aaa gaa gct cta tta gay aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30

|  |     |
|--|-----|
| tta gaa gaa atg aat ttg cca ggr aga tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Met Asn Leu Pro Xaa Arg Trp Lys Pro Lys Met Ile Gly | 144 |
| 35 40 45   |     |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct rta<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Xaa | 192 |
| 50 55 60   |     |
| gaa att tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr | 240 |
| 65 70 75 80  |     |
| cct gtc aac ata att gga aga aat ctg atg act cag ctt ggc tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr | 288 |
| 85 90 95   |     |
| tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys | 336 |
| 100 105 110  |     |
| cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gag<br>Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu | 384 |
| 115 120 125  |     |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly | 432 |
| 130 135 140  |     |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe | 480 |
| 145 150 155 160  |     |
| gcc ata aag aaa aaa gac agt aat aga tgg aga aaa tta gtg gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Asn Arg Trp Arg Lys Leu Val Asp Phe | 528 |
| 165 170 175  |     |
| aga gaa ctt aat aar aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly | 576 |
| 180 185 190  |     |
| ata cca cat cct gca ggg tta raa aag aac aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu | 624 |
| 195 200 205  |     |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg | 672 |
| 210 215 220  |     |
| aag tat act gca ttt acc ata cct agt acc aat aat gag aca ccm ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Xaa Gly | 720 |
| 225 230 235 240  |     |
| gtt aga tat cag tat aat gta ctt ccc cag gga tgg aaa gga tca cca<br>Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro | 768 |
| 245 250 255  |     |
| gca tat tty caa tgt agy atg aca aaa atc tta aag cct ttc agg aaa<br>Ala Tyr Phe Gln Cys Xaa Met Thr Lys Ile Leu Lys Pro Phe Arg Lys | 816 |
| 260 265 270  |     |
| caa aat cca cac ata gtt att ttt caa tat gtg gat gac ttg tat gta<br>Gln Asn Pro His Ile Val Ile Phe Gln Tyr Val Asp Asp Leu Tyr Val | 864 |
| 275 280 285  |     |

gca tct gac tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg 912  
 Ala Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu  
 290 295 300

aga caa cat ttg ttg agg tgg gga ctc acc aca cca gac aaa aaa cat 960  
 Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

caa aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag ccc ata acg ctg cca gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Thr Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tat gca ggg 1116  
 Ile Tyr Ala Gly  
 370

<210> 61

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1)...(297)

<223> HIV Protease

<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

<400> 61

cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gat agg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Asp Arg  
 1 5 10 15

ggg gca agt aaa gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Ala Ser Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa ata aat ttg cca ggg rag tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Ile Asn Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tmt gat cag ata ccc gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Xaa Asp Gln Ile Pro Val  
 50 55 60

gaa att tgt gga cat aag gct ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr  
 85 90 95

|   |      |
|---|------|
| tta aat ttt ccc atc agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336  |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt cag tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa agc ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Ser Phe Arg<br>210 215 220     | 672  |
| aag tac act gca ttt acc ata ccc agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| rca aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gaa atg gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gag ata gag caa cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |

```

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tat cca ggg
Ile Tyr Pro Gly
      370

<210> 62
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 62
cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
      20                      25                      30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aga caa tat gat cag ata gcc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile
      50                      55                      60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg atg act cag att ggc tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

```

gcc ata aag aaa aag aat agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc gca ggg cta aaa aag aay aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtc ccc tta gat gaa gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg  
 210 215 220

aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240

rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
 Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255

tca ata ttc caa tgt agc atg acg aaa atc tta gag cct ttt aga aaa 816  
 Ser Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
 260 265 270

cag aat cca gac ata gtt atc trt caa tac atg gat gat ttg tat gta 864  
 Gln Asn Pro Asp Ile Val Ile Xaa Gln Tyr Met Asp Asp Leu Tyr Val  
 275 280 285

gca tct gac tta gaa ata gag cag cat aga ata aaa ata gag gaa cta 912  
 Ala Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu Glu Leu  
 290 295 300

aga caa cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aaa yat 960  
 Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys Xaa  
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gar ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag ttr gtg gga aaa ctg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Xaa Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tac cca ggg 1116  
 Ile Tyr Pro Gly  
 370

&lt;210&gt; 63

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 63
cct caa atc act ctt tgg caa cga ccc gtt gtt aca gta agg ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Val Arg Ile Gly
  1              5              10              15

gga cag cta acg gaa gct yta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
              20              25              30

tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly
              35              40              45

ggr att gga ggt ttt atc aaa gta aga cag tat gat cac gta ctt gta      192
Xaa Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp His Val Leu Val
              50              55              60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
  65              70              75              80

cct gtc aac ata att gga aga aat ttg atg act cag ctt ggg ttc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr
              85              90              95

tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
              100              105              110

cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg mca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Xaa Glu Glu
              115              120              125

aaa ata aaa gca cta aca gaa att tgt aca gaa ttg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
              130              135              140

aaa att tca aga ata ggg cct gaa aat cca tac aat act cca ata ttt      480
Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
  145              150              155              160

gcc ata aag aag aaa aac ggt ayt agg tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Gly Xaa Arg Trp Arg Lys Leu Val Asp Phe
              165              170              175

aga gag cta aat aag aga act caa gac ttc tgg gaa gtt caa cta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
              180              185              190

ata cca cat cct gca gga cta aaa aag aac aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
              195              200              205

gat gtg ggt gat gca tat ttt tca gtt ccc tta cat gaa gac ttt aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu His Glu Asp Phe Arg
  210              215              220

```

```

aag tat acc gca ttc acc ata cct agt aca aac aat gaa aca cca gga      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
225                      230                      235                      240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca ccg      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                      245                      250                      255

gca ata ttc caa agt agc atg acc aaa atc tta gaa cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                      260                      265                      270

caa aat cca gaa atg gtt atc tat caa tac gtg gat gat ttg tat gta      864
Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val
                      275                      280                      285

gga tct gac tta gaa ata ggg cag cat aga ata aaa ata gag gaa tta      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ile Lys Ile Glu Glu Leu
                      290                      295                      300

agg gaa cac cta ttg aag tgg gga ttt ttc acc cca gac gaa aag cat      960
Arg Glu His Leu Leu Lys Trp Gly Phe Phe Thr Pro Asp Glu Lys His
305                      310                      315                      320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctt cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gtg cag cct ata aaa ctg cca gaa aaa gaa agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Glu Ser Trp Thr
                      340                      345                      350

gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agc cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tat cca gga
Ile Tyr Pro Gly
370

```

```

<210> 64
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 64
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

```



|   |     |
|---|-----|
| tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa atr ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Xaa Ile Gly<br>35 40 45        | 144 |
| gga att gga ggy ttt rtc aaa gta aga cag tat gat cag ata syc ata<br>Gly Ile Gly Xaa Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile<br>50 55 60        | 192 |
| gaa atc tgc gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gyc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act<br>Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta caa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Gln Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aag ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gct ata aag aaa aag gac agt gct aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Ala Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cck cat ccc gca ggg ttr aaa aag aaa aaa tca gta aca gta cta<br>Ile Xaa His Pro Ala Gly Xaa Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624 |
| gat gta ggt gat gca tat ttt tca gtt ccc tta gat caa aac ttc aga<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asn Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttc acc ata cct agt ata aac aat gag ayg cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gar ata rtt atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Xaa Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

```

gga tct gac ttr gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Xaa Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
 290                      295                      300

aga caa cat ytg ttg aag tgg gga ttt acc aca cca gac aag aag cat      960
Arg Gln His Xaa Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
 305                      310                      315                      320

cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
 355                      360                      365

att tat gca gga
Ile Tyr Ala Gly
 370

```

```

<210> 65
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 65
cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
 1                      5                      10                      15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gac atc aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt gtc aaa gta aga gag tat gat cag gta ccc ata      192
Gly Ile Gly Gly Phe Val Lys Val Arg Glu Tyr Asp Gln Val Pro Ile
 50                      55                      60

gac atc tgt gga cat aaa gtt ata ggt aca gtg tta gta gga cct aca      240
Asp Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
 65                      70                      75                      80

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                      85                      90                      95

```

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336  |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gar atc tgt aca gaa ttg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aay cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Xaa<br>195 200 205         | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672  |
| aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240     | 720  |
| rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gat ttg gaa ata gag cag cat aga aca aaa ata gag gaa cta<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga gaa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat<br>Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata aag ytg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Lys Xaa Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
           355                                  360                                  365

att tat cca ggg 1116  
 ile Tyr Pro Gly  
           370

<210> 66  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 66  
 cct cag atc act ctt tgg caa cga ccc ctt gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
   1                                  5                                  10                                  15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gak rca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Xaa Xaa Val  
                                   20                                  25                                  30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
                                   35                                  40                                  45

gga att gga ggt ttt atc aaa gta agr car tat gac cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile  
   50                                  55                                  60

gaa atc tgt gga cag aaa gct ata ggt aca gta tta gta gga cct acm 240  
 Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Val Gly Pro Xaa  
   65                                  70                                  75                                  80

cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
                                   85                                  90                                  95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                                   100                                  105                                  110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu  
                                   115                                  120                                  125

aaa ata aaa gca tta gca gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Ala Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
   130                                  135                                  140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
   145                                  150                                  155                                  160

|   |      |
|---|------|
| gcc ata aag aaa aaa gac agt aat ara tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Asn Xaa Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| agg gaa ctc aat aag aga act caa gac ttc tgg gaa gtt caa tta ggc<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca rta ctr<br>Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Xaa Xaa<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aar tat act gca ttt acc ata cct agt aca wac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Xaa Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag krc aat gtg yyt cca cag gga tgg aaa gga tcm cca<br>Ile Arg Tyr Gln Xaa Asn Val Xaa Pro Gln Gly Trp Lys Gly Xaa Pro<br>245 250 255     | 768  |
| gca ata ttc mam agt agc ayg aca aaa att tta gag cct ttt aga aaa<br>Ala Ile Phe Xaa Ser Ser Xaa Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tgt caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ttg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| agg caa cat ttg ttg agg tgg ggr ttt acc aca cca gac ara aaa cat<br>Arg Gln His Leu Leu Arg Trp Xaa Phe Thr Thr Pro Asp Xaa Lys His<br>305 310 315 320 | 960  |
| cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata aaa ctg cca gaa aaa gay agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |

<210> 67  
 <211> 1119  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)  
 <220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1119)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 67
cct caa atc act ctt tgg caa cga cca ata gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1             5             10             15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

cta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
             35             40             45

gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata tcc ata      192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile
             50             55             60

gaa atc tgt ggg cat aaa gtt aca ggt aca gtg tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Val Thr Gly Thr Val Leu Ile Gly Pro Thr
             65             70             75             80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
             115            120            125

aaa ata aaa gca ttg gta gaa att tgt gca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Met Glu Lys Glu Gly
             130            135            140

caa att tca aaa att gag cct gaa aat cca tac aat aat cca gta ttt      480
Gln Ile Ser Lys Ile Glu Pro Glu Asn Pro Tyr Asn Asn Pro Val Phe
             145            150            155            160

gtc ata aag aaa aaa gac ggt act aac tgg aga aaa tta ata gat ytc      528
Val Ile Lys Lys Lys Asp Gly Thr Asn Trp Arg Lys Leu Ile Asp Xaa
             165            170            175

aga gaa ctt aat aag aga act caa gat ttc tgg gaa att caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly
             180            185            190

ata cca cat ccc gca ggg tta aaa aag aat aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca ttt tat tca gtt ccc tta gat gag aac ttc agg      672
Asp Val Gly Asp Ala Phe Tyr Ser Val Pro Leu Asp Glu Asn Phe Arg
             210            215            220

```

```

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

aac aat cca gac ata gtc atc tat caa tac atg gat gat ttg tat gta      864
Asn Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                               275                               280                               285

gca tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                               290                               295                               300

aga gaa cat cta ttr aag tgg gga ttt acc aca cca gac aar aar yat      960
Arg Glu His Leu Xaa Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys Xaa
305                               310                               315                               320

cag aaa gaa cct cca ytc ctt tgg atg ggt tat gaa ctc cat cct gat     1008
Gln Lys Glu Pro Pro Xaa Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act     1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag     1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg att
Ile Tyr Pro Gly Ile
                               370

```

```

<210> 68
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

```

```

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 68
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1                               5                               10                               15

gga caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

```

|   |     |
|---|-----|
| tta gaa gaa atg aat ttg cca ggg aaa tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga atc gga gga ttt atc aaa gta aga cag tat gag cag ata cac ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile His Ile<br>50 55 60        | 192 |
| gaa atc tgt ggg cat aaa gct ata ggt aca gtr tta ata gga ccc aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga<br>Lys Ile Lys Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140 | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtt ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat cct gca ggg ttg aag aag aaa aaa tca gta aca gta cta<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa aac ttt agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asn Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aat aat gaa aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa gct agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac atg rtt att tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |



```

ggc tct gac tta gaa ata gga cag cat aga aca aaa ata gaa gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
290                               295                               300

aga caa cat ctg ttg agg tgg ggg ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                               310                               315                               320

cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                               340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                               355                               360                               365

att tat cca ggg att
Ile Tyr Pro Gly Ile
370

```

```

<210> 69
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 69
cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
1                               5                               10                               15

ggg caa yta aag gaa gct mta tta gay aca gga gca gat gat aca gtg      96
Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
                               35                               40                               45

gga att gga ggt ttt atc aaa gta aga gag tat gag cag ata caa gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Glu Tyr Glu Gln Ile Gln Val
50                               55                               60

gaa atc tgt gga cat aag gct ata rgt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Xaa Thr Val Leu Ile Gly Pro Thr
65                               70                               75                               80

cct gtc aac ata att gga aga aat cta atg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
                               85                               90                               95

```

|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gag act gta ccg gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336  |
| cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat acy ccr gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Xaa Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata ccg cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctr<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Xaa<br>195 200 205         | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gaa cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat car tac atg gat gac ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg tkg agg tgg gga ttt tac aca cca gac aaa aaa cat<br>Arg Gln His Leu Xaa Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cac cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctr cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Xaa Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
           355                                  360                                  365

att tat tca ggg att 1119  
 Ile Tyr Ser Gly Ile  
           370

<210> 70  
 <211> 1119  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1119)  
 <223> Portion of HIV Reverse Transcriptase

<400> 70  
 cct caa atc act ctt tgg caa cga ccc cty gtc kca ata aag gta ggr 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Xaa Ile Lys Val Xaa  
           1                                  5                                  10                                  15

ggg caa mta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
                                   20                                  25                                  30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
           35                                  40                                  45

gga att gga ggt ttt atc aaa gta aaa cag tat gat cag gta arc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Xaa Ile  
           50                                  55                                  60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr  
           65                                  70                                  75                                  80

cct gtc aac ata att gga aga aay ctg ttg aca cag att ggt tgy act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
                                   85                                  90                                  95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                                   100                                  105                                  110

cca gga atg gat ggc cca ara gty aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Xaa Xaa Lys Gln Trp Pro Leu Thr Glu Glu  
           115                                  120                                  125

aaa ata aar gca tta atg gaa att tgt gca gay atg gaa aag gaa ggr 432  
 Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Asp Met Glu Lys Glu Xaa  
           130                                  135                                  140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
           145                                  150                                  155                                  160

|   |      |
|---|------|
| gcy ata aag aaa aaa gac agc act aaa tgg aga aaa tta gta gat ttc<br>Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aaa act caa gac ttt tgg gaa gtc caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccy gca ggg tta aaa aag aac aaa tca gta aca gta ttg<br>Ile Pro His Xaa Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aaa tay act gca ttt acm ata cct agt ata aat aat gca aca cca ggg<br>Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Ala Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga rar<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Xaa<br>260 265 270     | 816  |
| cag aat cca gac ata gtt atc tat caa tac atg gat gay ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa mta ggg cag cat aga rca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg tta agg tgg ggg ttt acc acw cca gac aag aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Thr Xaa Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta car ccc ata gtg ttg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tay gsa ggg att<br>Ile Tyr Xaa Gly Ile<br>370   | 1119 |

<210> 71  
 <211> 1119  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)  
 <220>

<221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1119)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 71
cct caa atc act ctt tgg caa cga ccc atc gtc tca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Ser Ile Lys Ile Gly
  1             5             10             15

ggg gca aat aaa gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
             20             25             30

tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg     144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
             35             40             45

gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata     192
Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
             50             55             60

gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca     240
Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr
             65             70             75             80

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act     288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
             85             90             95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag     336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
             100            105            110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag     384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu
             115            120            125

aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga     432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly
             130            135            140

aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt     480
Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
             145            150            155            160

gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc     528
Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
             165            170            175

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga     576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
             180            185            190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg     624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
             195            200            205

gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg     672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
             210            215            220

```

|   |      |
|---|------|
| aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat ccc gac ata gtt atc tat caa tac gtg gat gat ttg ctt gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat<br>Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gcw agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Xaa Ser Gln<br>355 360 365     | 1104 |
| att tat cca ggg att<br>Ile Tyr Pro Gly Ile<br>370   | 1119 |

<210> 72  
 <211> 1119  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1119)  
 <223> Portion of HIV Reverse Transcriptase

|   |    |
|---|----|
| <400> 72<br>cct cag atc act ctt tgg caa cga ccc cty gtc aca ata aag atc ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly<br>1 5 10 15 | 48 |
| ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta<br>Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val<br>20 25 30              | 96 |

|   |     |
|---|-----|
| ata gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg<br>Ile Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt rtc aaa gta aga caa tat gat cag gta ccc ata<br>Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Val Pro Ile<br>50 55 60        | 192 |
| gaa att tgc gga cat aaa gct ata ggt aca gta tta ata gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gyc aac ata att gga aga aac ctg ttg act caa ctt ggc tgc act<br>Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aaa gga agg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Gly Arg<br>130 135 140     | 432 |
| aaa aat tac aaa att ggg cct gaa aac cca tac aat act cca gta ttt<br>Lys Asn Tyr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624 |
| gat gtg ggt gat gca tat ttc tca gtt ccc tta gat aag gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctc cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gcm ata ttc caa tgt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Xaa Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |

|   |      |
|---|------|
| ggg tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga cga cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aaa cat<br>Arg Arg His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gag ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta caa cct ata gtg cta cca gag aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aag tta aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| ata tac gca ggg att<br>Ile Tyr Ala Gly Ile<br>370   | 1119 |
| <210> 73  |      |
| <211> 1119  |      |
| <212> DNA   |      |
| <213> Human Immunodeficiency Virus (HIV)  |      |
| <220>   |      |
| <221> CDS   |      |
| <222> (1)...(297)   |      |
| <223> HIV Protease  |      |
| <221> CDS   |      |
| <222> (298)...(1119)  |      |
| <223> Portion of HIV Reverse Transcriptase  |      |
| <400> 73  |      |
| cct caa atc act ctt tgg caa cga ccc ttc gtc aca gta aag ata ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Val Lys Ile Gly<br>1 5 10 15       | 48   |
| ggg cag cta aag gaa gct cta tta gat aca gga gca gat aat aca gta<br>Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val<br>20 25 30        | 96   |
| tta gaa gaa atg aat tta ccg gga aga tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45        | 144  |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile<br>50 55 60        | 192  |
| gaa atc tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr<br>65 70 75 80     | 240  |
| cct gtc aac ata att gga aga gat ctg ttg act cag ctt ggt tgc act<br>Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288  |



|   |      |
|---|------|
| tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aaa | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gaa ggg | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly |      |
| 130 135 140   |      |
| aag att tca aaa att ggg cct gaa aat cca tac aat acc cca gta ttt | 480  |
| Lys Ile Ser Lys Ile ggg cct gaa aat cca tac aat acc cca gta ttt |      |
| 145 150 155 160   |      |
| gct ata aag aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc | 528  |
| Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe |      |
| 165 170 175   |      |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |      |
| 180 185 190   |      |
| ata cca cat ccc gcg ggg tta aaa aag aac aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Asn Lys Ser Val Thr Val Leu     |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att aga tat cag tac aat gtg ctt ccc cag gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| cag aat cca gac ata gtt atc tac caa tac gtg gat gac ttg tat gta | 864  |
| Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gat gag ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Asp Glu Leu |      |
| 290 295 300   |      |
| agg caa cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aag cat | 960  |
| Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cca cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
                   355                                  360                                  365

att tac cca ggg att 1119  
 Ile Tyr Pro Gly Ile  
                   370

<210> 74  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 74  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag gtc ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly  
           1                                  5                                  10                                  15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
                   20                                  25                                  30

tta gag gaa cta aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Leu Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
                   35                                  40                                  45

gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile  
           50                                  55                                  60

gaa ata tgt gga cat aaa gct att ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
           65                                  70                                  75                                  80

cct gtc aac ata att gga aga aac ttg ttg act cag ctt ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr  
                   85                                  90                                  95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                   100                                  105                                  110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
                   115                                  120                                  125

aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
           130                                  135                                  140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
           145                                  150                                  155                                  160

|   |      |
|---|------|
| gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggt tta aaa aag aaa aaa tca gta aca gtc ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672  |
| aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tac cag tac aat gtg ctt ccc cag ggg tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt agg aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tac caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300         | 912  |
| aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gag ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gat agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |

&lt;210&gt; 75

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(819)

&lt;223&gt; Portion of HIV Reverse Transcriptase

&lt;400&gt; 75

|   |     |
|---|-----|
| ccc att agt cct att gam act gta cca gta aaa tta aag cca gga atg | 48  |
| Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys Pro Gly Met |     |
| 1 5 10 15   |     |
| gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa aaa ata aaa | 96  |
| Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys |     |
| 20 25 30  |     |
| gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga aaa att tca | 144 |
| Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser |     |
| 35 40 45  |     |
| aaa att ggg cct gaa aat cca tac aat act cca gta ttt gcc ata aag | 192 |
| Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys |     |
| 50 55 60  |     |
| aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc aga gaa ctt | 240 |
| Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu |     |
| 65 70 75 80   |     |
| aat aar aga act caa gat ttc tgg gaa gtt caa tta gga ata cca cat | 288 |
| Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His |     |
| 85 90 95  |     |
| ccc tca ggg tta aaa aag aay aaa tca gta aca gta ttg gat gtg ggt | 336 |
| Pro Ser Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu Asp Val Gly |     |
| 100 105 110   |     |
| gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg aag tat act | 384 |
| Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg Lys Tyr Thr |     |
| 115 120 125   |     |
| gca ttt acc ata cct agt ata aac aat gag aca cca ggg att agr tat | 432 |
| Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Xaa Tyr |     |
| 130 135 140   |     |
| cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca gca ata ttc | 480 |
| Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe |     |
| 145 150 155 160   |     |
| caa agt agc atg aca aaa atc tta gag cct ttt aga aaa cat aat cca | 528 |
| Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys His Asn Pro |     |
| 165 170 175   |     |
| gac ata gtt atc tat caa tac gtg gat gat ttg tat gta gga tct gac | 576 |
| Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp |     |
| 180 185 190   |     |
| tta gaa ata gag gag cat aga aca aaa ata gag gaa ctg agr vrg cat | 624 |
| Leu Glu Ile Glu Glu His Arg Thr Lys Ile Glu Glu Leu Xaa Xaa His |     |
| 195 200 205   |     |
| ctg tta aag tgg gga ttt acy aca cca gac aaa aag cat cag aaa gaa | 672 |
| Leu Leu Lys Trp Gly Phe Xaa Thr Pro Asp Lys Lys His Gln Lys Glu |     |
| 210 215 220   |     |
| cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat aaa tgg aca | 720 |
| Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr |     |
| 225 230 235 240   |     |

gta cag cct ata aag ctg cca gaa aaa gac agc tgg act gtc aat gac 768  
 Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp  
                   245                  250                  255

ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag att tat gca 816  
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala  
                   260                  265                  270

ggg 819  
 Gly

<210> 76

<211> 819

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (1)...(819)

<223> Portion of HIV Reverse Transcriptase

<400> 76

ccc att agt cct att gaa act gta cca gta aaa tta aag cca gga atg 48  
 Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met  
   1                  5                  10                  15

gat ggc cca aaa gty aaa caa tgg cca tta aca gaa gaa aaa ata aga 96  
 Asp Gly Pro Lys Xaa Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Arg  
                   20                  25                  30

gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga aaa att tca 144  
 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser  
                   35                  40                  45

aaa att ggg cct gaa aat cca tac aat act cca gtg ttt gct ata aag 192  
 Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys  
                   50                  55                  60

aaa aaa gac agt act aar tgg aga aaa ttg gta gat ttc aga gaa ctt 240  
 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu  
                   65                  70                  75                  80

aat aag aga act caa gac ttc tgg gaa gtt caa tta gga ata cca cat 288  
 Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His  
                   85                  90                  95

ccc tca ggg tta aaa aag aaa aaa tca gta aca gta ctg gat gtg ggt 336  
 Pro Ser Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly  
                   100                  105                  110

gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg aag tat act 384  
 Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr  
                   115                  120                  125

gca ttt act atn cct agt ata aac aat gag aca cca ggg att agg tat 432  
 Ala Phe Thr Xaa Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr  
                   130                  135                  140

cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca gca ata ttc 480  
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe  
                   145                  150                  155                  160

|   |     |
|---|-----|
| caa agt agc atg aca aaa atc tta gag cct ttt aga aaa caa aat cca | 528 |
| Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro |     |
| 165 170 175   |     |
| gac ata gtt atc tat caa tac gtg gat gat ttg tat gta gga tct gac | 576 |
| Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp |     |
| 180 185 190   |     |
| cta gaa ata gga cag cat aga aca aaa ata gag gaa ctg aga cag cat | 624 |
| Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His |     |
| 195 200 205   |     |
| ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat cag aaa gaa | 672 |
| Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu |     |
| 210 215 220   |     |
| cct ccc ttt ctt tgg atg ggc tat gaa ctc cat cct gat aaa tgg aca | 720 |
| Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr |     |
| 225 230 235 240   |     |
| gta cag cct ata gag ctg cca gac aag gat agc tgg act gtc aat gac | 768 |
| Val Gln Pro Ile Glu Leu Pro Asp Lys Asp Ser Trp Thr Val Asn Asp |     |
| 245 250 255   |     |
| ata cag aag tta gtg gga aaa tta aat tgg gca agt cag ata tat gca | 816 |
| Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala |     |
| 260 265 270   |     |
| ggg   | 819 |
| Gly   |     |

<210> 77  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|   |     |
|---|-----|
| <400> 77  |     |
| cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg | 48  |
| Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly |     |
| 1 5 10 15   |     |
| ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta | 96  |
| Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val |     |
| 20 25 30  |     |
| tta gaa gac atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg | 144 |
| Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly |     |
| 35 40 45  |     |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct ata | 192 |
| Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| gaa atc tgc gga cat aaa gct gta ggt aaa gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Val Gly Lys Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ctg ttg act caa ctt ggt tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gct ata aag aaa aaa aac agt act aga tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga acg caa gac ttc tgg gaa gtt caa nnn nnn<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Xaa Xaa<br>180 185 190     | 576 |
| nnn nnn nnn nnn nnn ggg twa aaa aag aaa aaa tca gta aca gta ctg<br>Xaa Xaa Xaa Xaa Gly Xaa Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205             | 624 |
| gat gta ggt gat gca tat ttc tca gtt cct cta gat aaa gac ttc aga<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tac act gca ttc acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gtg<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912 |
| aga caa cat ttg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960 |

```

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
          325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
          340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agc cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
          355                      360                      365

ata tat gca ggg
Ile Tyr Ala Gly
          370

<210> 78
<211> 1122
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1122)
<223> Portion of HIV Reverse Transcriptase

<400> 78
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1              5              10              15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20              25              30

tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35              40              45

gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile
          50              55              60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
          65              70              75              80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
          85              90              95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100              105              110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
          115              120              125

```



|   |      |
|---|------|
| aaa ata aaa gca ttg gta gaa ata tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat acr cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata arg aaa aaa gaa agc tct agc tct aaa tgg aga aaa tta gta<br>Ala Ile Xaa Lys Lys Glu Ser Ser Ser Lys Trp Arg Lys Leu Val<br>165 170 175         | 528  |
| gat ttc aga gaa ctt aat aar aga act caa gac ttt ttk gaa gtt caa<br>Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Xaa Glu Val Gln<br>180 185 190     | 576  |
| tta gga ata cca cat ccc gca ggg tta aag aag aaa aaa tca gya aca<br>Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Xaa Thr<br>195 200 205         | 624  |
| rta ttg gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gac<br>Xaa Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp<br>210 215 220     | 672  |
| ttc agg aag tat act gca ttt acc ata cct agt ata aac aat gag aca<br>Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr<br>225 230 235 240 | 720  |
| cca ggg att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga<br>Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly<br>245 250 255     | 768  |
| tca cca gct ata ttc caa agt agc atg aca aaa atc tta gag cct ttt<br>Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe<br>260 265 270     | 816  |
| aga aaa caa aat cca gay ata gtt atc tat caa tac atg gat gat ttg<br>Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu<br>275 280 285     | 864  |
| tat gta gga tct gay tta gaa ata gag cag cat aga ata aaa ata gag<br>Tyr Val Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu<br>290 295 300     | 912  |
| gaa ctg aga caa yat ytg tgg arg tgg ggr ttt tac aca cca gac aaa<br>Glu Leu Arg Gln Xaa Xaa Trp Xaa Trp Xaa Phe Tyr Thr Pro Asp Lys<br>305 310 315 320 | 960  |
| aaa cat cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat<br>Lys His Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His<br>325 330 335     | 1008 |
| cct gat aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc<br>Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser<br>340 345 350     | 1056 |
| tgg act gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca<br>Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala<br>355 360 365     | 1104 |
| agt cag att tat gca ggr<br>Ser Gln Ile Tyr Ala Xaa<br>370   | 1122 |

<210> 79  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 79  
 cct cag atc act ctt tgg caa cga ccc ctc gtt aca ata aag gta ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly  
 1 5 10 15  
 ggg caa cta aag gaa gct cta tta gat aca gga gca gac aat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val  
 20 25 30  
 ttc gaa gac ctg gat tta cca gga agg tgg aaa cca aaa atg ata ggg 144  
 Phe Glu Asp Leu Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta aaa cag tat gag cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Pro Ile  
 50 55 60  
 gaa atc tgt ggg cgt aaa gct ata ggt aca gtg tta gta gga cct aca 240  
 Glu Ile Cys Gly Arg Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80  
 cct gtc aac ata att gga aga gat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95  
 cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta ata gaa att tgt gca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Ala Glu Met Glu Lys Glu Gly  
 130 135 140  
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aag aac agt aat aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Ser Asn Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175  
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

|   |      |
|---|------|
| ata cca cat ccc gca ggg tta aaa aag aaa aag tca ata aca gta tta<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Ile Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gat tta gaa ata gag cag cat aga aca aaa ata gat gaa ctg<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg agg tgg gga ctt acc aca cca gac cag aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Gln Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gac aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg ggr aaa ttg aat tgg gca agt caa<br>Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tac cca ggg<br>Ile Tyr Pro Gly<br>370   | 1116 |

<210> 80  
 <211> 1119  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1119)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 80
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1                               5                               10                               15

ggg cag cta aag gag gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                               20                               25                               30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                               35                               40                               45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
                               50                               55                               60

gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
   65                               70                               75                               80

cct gtc aac ata att gga aga aat ctg ttg acw cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Xaa Gln Ile Gly Cys Thr
                               85                               90                               95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                               100                              105                              110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
                               115                              120                              125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aar gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                               130                              135                              140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca rta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Xaa Phe
                               145                              150                              155                              160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                               165                              170                              175

aga gaa ctt aat aag agg act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                               180                              185                              190

ata cca cat ccc gca ggg ttg aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
                               195                              200                              205

gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
                               210                              215                              220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
                               225                              230                              235                              240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                              250                              255

```

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816  
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
 260 265 270

caa aat cca gac ata gtc atc tat caa tac atg gat gat ttg tat gta 864  
 Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
 275 280 285

gga tct gac tta gaa ata ggg cag cat agg aca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu  
 290 295 300

aga caa cat ttg ttg aag tgg ggg ttt acc aca cca gac aaa aaa cat 960  
 Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gtg cag cct ata gtg tta ccg gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tac cca ggg att 1119  
 Ile Tyr Pro Gly Ile  
 370

<210> 81  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 81  
 cct caa atc act ctt tgg caa cga ccy ctt gtt rcc ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Xaa Leu Val Xaa Ile Lys Ile Gly  
 1 5 10 15

ggg caa cta arg gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Xaa Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aaa cag tat gat caa ata ccy rta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Xaa Xaa  
 50 55 60

|   |     |
|---|-----|
| gaa att tgt gga cat aga gct ata ggt aca gtw tta gta gga cct aca<br>Glu Ile Cys Gly His Arg Ala Ile Gly Thr Xaa Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga agr aat ctg ttg act cag att ggt tgc act<br>Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aga att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gct ata aag aaa aar gat agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| agg gaa ctt aat aag agg act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cca ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa yta<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa<br>290 295 300     | 912 |
| aga gaa cat ctg tta arg tgg gga ttt acc aca cca gac aaa aag cat<br>Arg Glu His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960 |

```

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat    1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gta cag cct ata cag ctg cca gaa aag gaa agc tgg act    1056
Lys Trp Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Glu Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag    1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tat gca ggg
Ile Tyr Ala Gly
                      370

<210> 82
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 82
cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg    48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
1                      5                      10                      15

ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta    96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val
                      20                      25                      30

tta gaa gaa atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg    144
Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta    192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val
50                      55                      60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca    240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65                      70                      75                      80

ccc gtc aac ata att gga aga aat ctg ttg act cag att ggg tgc act    288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag    336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa    384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115                      120                      125

```

|   |      |
|---|------|
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aaa aag aaa gac agt act aaa tgg aga aag tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aay aaa aag act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205         | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gam ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Xaa Phe Arg<br>210 215 220     | 672  |
| aar tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tay cag tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggr aag cac aga aca aaa ata gag gag cta<br>Gly Ser Asp Leu Glu Ile Xaa Lys His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga cag cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctk tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata aaa ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gty aat gac ata cag aag tta gtg gga aaa ttr aat tgg gcc agt cag<br>Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |



<210> 83  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 83
cct cag atc act ctt tgg caa cga cca ctc gtc gca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly
  1               5               10               15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20               25               30

tta gaa gac atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                35               40               45

gga att gga ggt ttt atc aaa gta aga cag tat gat caa gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
  50               55               60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
  65               70               75

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                85               90               95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                100              105              110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                115              120              125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
                130              135              140

aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
                145              150              155

gcc ata aag aaa aaa gac agt act aaa tgg agg aaa tta gta gat ttt      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                165              170              175

aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                180              185              190

```

|   |      |
|---|------|
| ata cca cat cca gca ggg tta aaa aag aaa aag tca gta aca gtg ctg | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata ccc agt ata aac aat gag aca ccc agg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Arg |      |
| 225 230 235 240   |      |
| gtt aga tat caa tac aat gta ctt cca cag gga tgg aaa gga tca cca | 768  |
| Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca tat ttc caa agt agc atg aca aaa atc tta gaa ccc ttc aga aaa | 816  |
| Ala Tyr Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aac cca gac ata gtt atc tat caa tac atg gat gac tta tat gta | 864  |
| Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gag ata gga cag cat aga gca aaa ata gag gac cta | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Asp Leu |      |
| 290 295 300   |      |
| aga gca cat ctg ttg aag tgg ggg ttt acc aca cca gac aaa aaa cat | 960  |
| Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa ccc cca ttt ctc tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta cag cct ata gwg cta cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |
| gtc aat gac ata cag aaa tta gta gga aaa tta aat tgg gca agt cag | 1104 |
| Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln |      |
| 355 360 365   |      |
| att tat cca ggg   | 1116 |
| Ile Tyr Pro Gly   |      |
| 370   |      |

<210> 84  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

```

<400> 84
cct caa atc act ctt tgg caa cga ccc att gtc aca ata aaa gta ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Val Gly
  1           5           10           15

ggg caa cta atg gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Met Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
           20           25           30

tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa ata ata ggg      144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
           35           40           45

gga att ggt ggt ttt gtc aaa gtg aga cag tat gat cag gta ccc ata      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile
           50           55           60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
           65           70           75           80

cct acc aac gta gtt gga aga aat ctg atg act cag att ggc tgc acy      288
Pro Thr Asn Val Val Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Xaa
           85           90           95

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
           100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg acg gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
           115          120          125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat gga      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
           130          135          140

aaa att tca aaa att ggg cct gaa aat cca tat aat act cca ata ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
           145          150          155          160

gcc ata aag aaa aag aac agt gat aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Leu Val Asp Phe
           165          170          175

aga gaa ctt aat aar aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
           180          185          190

ata cca cat cct gca ggg tta aaa aag aat aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
           195          200          205

gat ata ggt gat gca tat ttt tca att ccc tta gat aaa gac ttt agg      672
Asp Ile Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
           210          215          220

aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
           225          230          235          240

gtt aga tat cag tac aat gtg ctt cca cag gga tgg aag gga tca cca      768
Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
           245          250          255

```

gca ata ttc caa agc agc atg acc aaa atc tta gag cct ttt aga aaa 816  
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
                   260                                  265                                  270

cag aat cca gac ata gtt atc tgc caa tac gtg gat gat ttg tat gta 864  
 Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Val Asp Asp Leu Tyr Val  
                   275                                  280                                  285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctr 912  
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Xaa  
                   290                                  295                                  300

agg aat yat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa tat 960  
 Arg Asn Xaa Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys Tyr  
                   305                                  310                                  315                                  320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
   325                                  330                                  335

aaa tgg aca gta cag ccc ata gtg ctg cca gaa aaa gac agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
   340                                  345                                  350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
                   355                                  360                                  365

att tat cca ggg 1116  
 Ile Tyr Pro Gly  
                   370

<210> 85  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 85  
 cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aaa gta ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Val Gly  
           1                                  5                                  10                                  15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
                   20                                  25                                  30

tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
                   35                                  40                                  45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta agc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Ile  
           50                                  55                                  60

|   |     |
|---|-----|
| gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga ccc acc<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggr<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aar aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aaa ara act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Xaa Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gay gtg ggt gat gcr tat ttt tca gtt ccy tta gay aaa gay ttc agg<br>Asp Val Gly Asp Xaa Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aag tac aca gca ttt acc ata cct agt gta aac aat gag rca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Xaa Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca car gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aar<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| maa aat cca gac ata gty atc tay caa tac atg gat gat ttr tat gta<br>Xaa Asn Pro Asp Ile Xaa Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val<br>275 280 285     | 864 |
| gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912 |
| aga caa cat ctg ttg cag tgg ggg tta acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Gln Trp Gly Leu Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960 |

|   |      |
|---|------|
| cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat ccg gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335 | 1008 |
| aaa tgg aca gta cag cct ata wtg ctg cca gac aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Asp Lys Asp Ser Trp Thr<br>340 345 350 | 1056 |
| gtm aat gac ata cag aar tta gta gga aaa ttg aat tgg gcg agt cag<br>Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365 | 1104 |
| atc tac cca ggg<br>Ile Tyr Pro Gly<br>370   | 1116 |
| <210> 86  |      |
| <211> 1116  |      |
| <212> DNA   |      |
| <213> Human Immunodeficiency Virus (HIV)  |      |
| <220>   |      |
| <221> CDS   |      |
| <222> (1)...(297)   |      |
| <223> HIV Protease  |      |
| <221> CDS   |      |
| <222> (298)...(1116)  |      |
| <223> Portion of HIV Reverse Transcriptase  |      |
| <400> 86  |      |
| cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Gly<br>1 5 10 15   | 48   |
| ggg cac aca acg gaa gct cta tta gat aca gga gca gat gat aca gta<br>Gly His Thr Thr Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val<br>20 25 30        | 96   |
| tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata gga<br>Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45    | 144  |
| gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile<br>50 55 60    | 192  |
| gaa ttc tgt gga cat aaa act gta ggt aca gta tta ata gga cct aca<br>Glu Phe Cys Gly His Lys Thr Val Gly Thr Val Leu Ile Gly Pro Thr<br>65 70 75 80 | 240  |
| cct gtc aac ata att gga aga aat ctg atg act cag att ggt tgt act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr<br>85 90 95    | 288  |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110 | 336  |
| cca gga atg gat ggg ccc aaa gtt aaa cca tgg cca ttg aca gaa aga<br>Pro Gly Met Asp Gly Pro Lys Val Lys Pro Trp Pro Leu Thr Glu Arg<br>115 120 125 | 384  |

|   |      |
|---|------|
| aaa aat aaa gca tta gta gaa att tgt tcc gaa atg gaa aaa gga agg<br>Lys Asn Lys Ala Leu Val Glu Ile Cys Ser Glu Met Glu Lys Gly Arg<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gag aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt cag tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta aaa aag aac aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gta ggt gat gca tat ttt tca gtt ccc tta gat gaa gaa ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Glu Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttc acc ata cct agt aca aac aat gaa aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa tgt agc atg aca aaa atc tta gag ccc ttt aga aaa<br>Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gaa ata gtt atc tgt cag tac atg gat gac ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gca tct gat tta gaa ata ggg cag cat aga aca aaa gta gag gaa ctg<br>Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg aag tgg ggg ttt ttc aca cca gac gaa aaa cat<br>Arg Gln His Leu Leu Lys Trp Gly Phe Phe Thr Pro Asp Glu Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gta ctg cca gac caa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Gln Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agt caa<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tac cca ggg<br>Ile Tyr Pro Gly<br>370   | 1116 |

<210> 87  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 87  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata gag 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Glu  
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa atg aat ttg tca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Ser Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60

gag atc tgt gga cat aaa gct gta ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga agr aat ctg ttg act cag att ggt tgc acc 288  
 Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe  
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat tty 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190



|   |      |
|---|------|
| ata cca cat ccy gca ggg ttg aar aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Xaa Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gay ttc aga<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| gtt aga tat car tac aat gtg ctt cca cag gga tgg aag gga tca cca<br>Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt agg aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gat ata gtt atc tat caa tac atg gat gac ttr tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg car cat aga aca aaa ata gag gaa ttg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg aag tgg gga tta acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Lys Trp Gly Leu Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gat ata cag aag tta gtg gga aaa tta aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |

<210> 88  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 88

|   |     |
|---|-----|
| cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg | 48  |
| Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly |     |
| 1 5 10 15   |     |
| ggg caa cta agg raa gct cta tta gat aca gga gca gat gat aca gta | 96  |
| Gly Gln Leu Arg Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val |     |
| 20 25 30  |     |
| tta gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg | 144 |
| Leu Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly |     |
| 35 40 45  |     |
| gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata | 192 |
| Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile |     |
| 50 55 60  |     |
| gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca | 240 |
| Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr |     |
| 65 70 75 80   |     |
| cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act | 288 |
| Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr |     |
| 85 90 95  |     |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag | 336 |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |     |
| 100 105 110   |     |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gaa | 384 |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu |     |
| 115 120 125   |     |
| aaa ata gaa gca tta atr gaa att tgt gma ttt ttg gaa aag gaa gga | 432 |
| Lys Ile Glu Ala Leu Xaa Glu Ile Cys Xaa Phe Leu Glu Lys Glu Gly |     |
| 130 135 140   |     |
| aaa att tca aaa att ggg cct gaa aat ccg tac aac act cca gta ttt | 480 |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |     |
| 145 150 155 160   |     |
| gcc ata aag aaa aaa gga ggt act aaa tgg aga aaa ata gta gat ttc | 528 |
| Ala Ile Lys Lys Lys Gly Gly Thr Lys Trp Arg Lys Ile Val Asp Phe |     |
| 165 170 175   |     |
| aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga | 576 |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |     |
| 180 185 190   |     |
| ata cca cat ccc gcg ggg tta aaa aag aay aaa tca gta aca gta ctg | 624 |
| Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu |     |
| 195 200 205   |     |
| gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ctc agg | 672 |
| Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Leu Arg |     |
| 210 215 220   |     |
| aag tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg | 720 |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly |     |
| 225 230 235 240   |     |
| att aga tac caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca | 768 |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |     |
| 245 250 255   |     |

gca ata ttt caa agt agc atg aca aaa atc tta gag ccc ttt aga aag 816  
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
260 265 270

caa aat cca gac ata gtt atc twt caw tac gtg gat gat ttg tat gta 864  
Gln Asn Pro Asp Ile Val Ile Xaa Xaa Tyr Val Asp Asp Leu Tyr Val  
275 280 285

gga tct gac tta gaa ata ggg aag cat agg gaa aaa ata gag gaa ctg 912  
Gly Ser Asp Leu Glu Ile Gly Lys His Arg Glu Lys Ile Glu Glu Leu  
290 295 300

aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac gaa aaa cat 960  
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Glu Lys His  
305 310 315 320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ctt gat 1008  
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Leu Asp  
325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act 1056  
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365

att tat gca ggg 1116  
Ile Tyr Ala Gly  
370

<210> 89  
<211> 1116  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease

<221> CDS  
<222> (298)...(1116)  
<223> Portion of HIV Reverse Transcriptase

<400> 89  
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48  
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30

tta gaa gaa atg agt ttg cca ggg aga tgg aaa cca aaa atg ata ggg 144  
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
35 40 45

gga att gga ggt ttt atc aaa gta aga caa ttt gat cag ata ccc ata 192  
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Phe Asp Gln Ile Pro Ile  
50 55 60

|                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| gaa<br>Glu<br>65  | ata<br>Ile | tgt<br>Cys        | gga<br>Gly        | cac<br>His        | aaa<br>Lys<br>70  | gct<br>Ala        | ata<br>Ile        | ggt<br>Gly        | aca<br>Thr<br>75  | gta<br>Val<br>75  | tta<br>Leu        | ata<br>Ile        | gga<br>Gly        | cct<br>Pro        | aca<br>Thr<br>80  | 240 |
| cct<br>Pro        | gtc<br>Val | aac<br>Asn        | ata<br>Ile        | att<br>Ile<br>85  | gga<br>Gly        | agg<br>Arg        | aat<br>Asn        | ctg<br>Leu<br>90  | ttg<br>Leu        | act<br>Thr        | cag<br>Gln        | ctt<br>Leu        | ggt<br>Gly        | tgc<br>Cys<br>95  | act<br>Thr        | 288 |
| tta<br>Leu        | aat<br>Asn | ttt<br>Phe        | ccc<br>Pro<br>100 | atc<br>Ile        | agt<br>Ser        | cct<br>Pro        | att<br>Ile        | gaa<br>Glu<br>105 | cct<br>Pro        | gta<br>Val        | cca<br>Pro        | gta<br>Val        | aaa<br>Lys<br>110 | tta<br>Leu        | aag<br>Lys        | 336 |
| cca<br>Pro        | gga<br>Gly | atg<br>Met<br>115 | gat<br>Asp        | ggc<br>Gly        | cca<br>Pro        | aaa<br>Lys        | ggt<br>Val<br>120 | aaa<br>Lys        | caa<br>Gln        | tgg<br>Trp        | cca<br>Pro        | ttg<br>Leu<br>125 | aca<br>Thr        | gaa<br>Glu        | gaa<br>Glu        | 384 |
| aaa<br>Lys<br>130 | ata<br>Ile | aaa<br>Lys        | gca<br>Ala        | tta<br>Leu        | gta<br>Val<br>135 | gaa<br>Glu<br>135 | att<br>Ile        | tgt<br>Cys        | aca<br>Thr        | gaa<br>Glu<br>140 | ctg<br>Leu        | gaa<br>Glu        | aaa<br>Lys        | gaa<br>Glu        | ggg<br>Gly        | 432 |
| aaa<br>Lys<br>145 | att<br>Ile | tca<br>Ser        | aaa<br>Lys        | att<br>Ile<br>150 | ggg<br>Gly        | cct<br>Pro        | gaa<br>Glu        | aat<br>Asn        | cca<br>Pro        | tac<br>Tyr<br>155 | aat<br>Asn        | act<br>Thr        | cca<br>Pro        | ata<br>Ile        | ttt<br>Phe<br>160 | 480 |
| gcc<br>Ala        | ata<br>Ile | aag<br>Lys        | aaa<br>Lys<br>165 | aaa<br>Lys        | gac<br>Asp        | agt<br>Ser        | act<br>Thr        | aaa<br>Lys        | tgg<br>Trp<br>170 | aga<br>Arg        | aaa<br>Lys        | tta<br>Leu        | gta<br>Val        | gat<br>Asp<br>175 | ttc<br>Phe        | 528 |
| aga<br>Arg        | gaa<br>Glu | ctg<br>Leu<br>180 | aat<br>Asn        | aag<br>Lys        | aaa<br>Lys        | act<br>Thr        | caa<br>Gln        | gac<br>Asp<br>185 | ttc<br>Phe        | tgg<br>Trp        | gaa<br>Glu        | gtt<br>Val        | caa<br>Gln<br>190 | tta<br>Leu        | gga<br>Gly        | 576 |
| ata<br>Ile        | cca<br>Pro | cat<br>His<br>195 | ccc<br>Pro        | gca<br>Ala        | ggg<br>Gly        | tta<br>Leu        | aaa<br>Lys<br>200 | aag<br>Lys        | aaa<br>Lys        | aaa<br>Lys        | tca<br>Ser        | gta<br>Val<br>205 | acg<br>Thr        | gta<br>Val        | ctg<br>Leu        | 624 |
| gat<br>Asp<br>210 | gtg<br>Val | ggt<br>Gly        | gat<br>Asp        | gca<br>Ala        | tat<br>Tyr<br>215 | ttt<br>Phe        | tca<br>Ser        | gtt<br>Val        | ccc<br>Pro        | tta<br>Leu        | gat<br>Asp<br>220 | aaa<br>Lys        | gac<br>Asp        | ttc<br>Phe        | agg<br>Arg        | 672 |
| aaa<br>Lys<br>225 | tat<br>Tyr | act<br>Thr        | gca<br>Ala        | ttt<br>Phe        | acc<br>Thr<br>230 | ata<br>Ile        | cct<br>Pro        | agt<br>Ser        | aca<br>Thr        | aac<br>Asn<br>235 | aat<br>Asn        | gag<br>Glu        | aca<br>Thr        | cca<br>Pro        | ggg<br>Gly<br>240 | 720 |
| att<br>Ile        | aga<br>Arg | tat<br>Tyr        | cag<br>Gln        | tac<br>Tyr<br>245 | aat<br>Asn        | gtg<br>Val        | ctt<br>Leu        | cca<br>Pro        | cag<br>Gln<br>250 | gga<br>Gly        | tgg<br>Trp        | aaa<br>Lys        | gga<br>Gly        | tca<br>Ser<br>255 | cca<br>Pro        | 768 |
| gca<br>Ala        | ata<br>Ile | ttt<br>Phe        | caa<br>Gln<br>260 | cat<br>His        | agc<br>Ser        | atg<br>Met        | aca<br>Thr        | aaa<br>Lys<br>265 | atc<br>Ile        | tta<br>Leu        | gag<br>Glu        | cct<br>Pro        | ttt<br>Phe<br>270 | aga<br>Arg        | aaa<br>Lys        | 816 |
| cag<br>Gln        | aat<br>Asn | cca<br>Pro<br>275 | gac<br>Asp        | ata<br>Ile        | gtt<br>Val        | atc<br>Ile        | tat<br>Tyr<br>280 | caa<br>Gln        | tac<br>Tyr        | gtg<br>Val        | gat<br>Asp        | gac<br>Asp<br>285 | ttg<br>Leu        | tat<br>Tyr        | gta<br>Val        | 864 |
| gga<br>Gly<br>290 | tct<br>Ser | gac<br>Asp        | tta<br>Leu        | gaa<br>Glu        | ata<br>Ile        | ggg<br>Gly<br>295 | cag<br>Gln        | cat<br>His        | aga<br>Arg        | aca<br>Thr        | aaa<br>Lys<br>300 | ata<br>Ile        | gag<br>Glu        | gaa<br>Glu        | ctg<br>Leu        | 912 |
| aga<br>Arg<br>305 | gaa<br>Glu | cat<br>His        | ctg<br>Leu        | ttg<br>Leu        | aag<br>Lys<br>310 | tgg<br>Trp        | gga<br>Gly        | ttt<br>Phe        | tac<br>Tyr        | aca<br>Thr<br>315 | cca<br>Pro        | gac<br>Asp        | aaa<br>Lys        | aaa<br>Lys        | cat<br>His<br>320 | 960 |

|   |      |
|---|------|
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335 | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350 | 1056 |
| gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365 | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |
| <br><210> 90<br><211> 1116<br><212> DNA<br><213> Human Immunodeficiency Virus (HIV)   |      |
| <br><220><br><221> CDS<br><222> (1)...(297)<br><223> HIV Protease   |      |
| <br><221> CDS<br><222> (298)...(1116)<br><223> Portion of HIV Reverse Transcriptase   |      |
| <br><400> 90  |      |
| cct cag atc act ctt tgg caa cga ccc atg gtc aca ata aaa gta ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly<br>1 5 10 15   | 48   |
| gga cag cta aag gaa gct yta tta gat aca gga gca gat gat aca gta<br>Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Thr Val<br>20 25 30        | 96   |
| tta gaa gaa atg aac ttg cca gga aaa tgg aaa cca aaa ata ata ggg<br>Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly<br>35 40 45    | 144  |
| gga att gga ggt ttt gtc aga gta aga caa tat gat cag gta cct gta<br>Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Asp Gln Val Pro Val<br>50 55 60    | 192  |
| gaa att tgt gga cat aaa gct ata ggt tca gta tta gta gga cca aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr<br>65 70 75 80 | 240  |
| cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt ttc act<br>Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr<br>85 90 95    | 288  |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110 | 336  |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125 | 384  |

|   |      |
|---|------|
| aaa ata aaa gca tta gta gar att tgt aca gaa ytg gaa aaa gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Lys Glu Gly<br>130 135 140     | 432  |
| aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat cct gga ggg tta aaa aag aaa aaa tca gta aca gta cta<br>Ile Pro His Pro Gly Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata tty caa agt agc atg aca aaa atc tta gag cct ttt agg aag<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| maa aat cca gac ata gtt atc att caa tac atg gat gat ttg tat gtr<br>Xaa Asn Pro Asp Ile Val Ile Ile Gln Tyr Met Asp Asp Leu Tyr Xaa<br>275 280 285     | 864  |
| gga tct gat tta gaa ata gar cag cay aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga gat cat tta ttg agg tgg ggg ttt ttc aca cca gaa caa aaa cat<br>Arg Asp His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cat cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val His Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa ttr aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |

<210> 91  
 <211> 1115  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1115)  
 <223> Portion of HIV Reverse Transcriptase

<400> 91  
 cct cag atc act ctt tgg caa cga ccc ctt gtc aca gta aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly  
 1 5 10 15  
 ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30  
 ttg gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60  
 gaa atc tgt gga cat aaa gtt ata rgt cca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Val Ile Xaa Pro Val Leu Ile Gly Pro Thr  
 65 70 75 80  
 cct gtc aac ata att gga aga aat ttg atg act cag att ggc tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc atc agt cct att raa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Xaa Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aag gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140  
 aaa atc tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aaa aac agt act aga tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe  
 165 170 175  
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

|   |      |
|---|------|
| ata cca cat cct gga ggg tta aaa aag aaa aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Gly Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt cct cta gat gaa gac ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| gtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcg cca | 768  |
| Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttt cag gct agc atg aca aaa atc tta gag ccg ttt aga aaa | 816  |
| Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac cta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga caa cat ttg ttg aaa tgg gga ttt atc aca cca gat gaa aaa cat | 960  |
| Arg Gln His Leu Leu Lys Trp Gly Phe Ile Thr Pro Asp Glu Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aag tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |
| gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag | 1104 |
| Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln |      |
| 355 360 365   |      |
| att tat gca gg  | 1115 |
| Ile Tyr Ala   |      |
| 370   |      |

<210> 92  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase



<400> 92  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
 1 5 10 15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gac ata aac ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Asp Ile Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile  
 50 55 60

gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ctg atg act cag att ggg tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa .caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcc ata aag aaa aag aac agt act aga tgg aga aaa gta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Val Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aac aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg  
 210 215 220

aag tat act gca ttt acc ata cct agt ata aac aat gag acg cca ggg 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240

att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255

|   |      |
|---|------|
| gca ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac ctg gtt atc tgt caa tac atg gat gat tta tat gta | 864  |
| Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac cta gaa ata ggg cag cat aga aca aaa ata gaa gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| agg caa cat ctg ttg aag tgg gga ttt acc aca cca gac gaa aaa cat | 960  |
| Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Glu Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta cag ccc ata gtg ctg cca gac aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Asp Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag | 1104 |
| Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln |      |
| 355 360 365   |      |
| att tat gca ggg   | 1116 |
| Ile Tyr Ala Gly   |      |
| 370   |      |

<210> 93  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|   |     |
|---|-----|
| <400> 93  |     |
| cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata gga | 48  |
| Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly |     |
| 1 5 10 15   |     |
| ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gta | 96  |
| Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val |     |
| 20 25 30  |     |
| tta gaa gaa atg aat tta cca gga aga tgg aca cca aaa ata ata ggg | 144 |
| Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Thr Pro Lys Ile Ile Gly |     |
| 35 40 45  |     |
| gga att gga ggt ttt gtc aga gta aga cag tat gaa cag ata ccc gta | 192 |
| Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Glu Gln Ile Pro Val |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| gaa atc tgc ggg cat aaa gct gta ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgt act<br>Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca ara gtt aaa caa tgg cca ttg aca gaa gag<br>Pro Gly Met Asp Gly Pro Xaa Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gam gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Xaa Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gct ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat cct gca ggg ata maa aag aac aaa tca gta aca gta ytg<br>Ile Pro His Pro Ala Gly Ile Xaa Lys Asn Lys Ser Val Thr Val Xaa<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gag gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672 |
| aag tac act gca ttt acc ata cct agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gta ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa aty tta gag cct ttt aga aag<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Xaa Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| aaa aat cca gac ata rtt atc tgc caa tac atg gat gat ttg tat gta<br>Lys Asn Pro Asp Ile Xaa Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| gga tct gac tta gaa ata gag cag cat aga aca aaa ata gat gaa ctg<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Asp Glu Leu<br>290 295 300     | 912 |
| aga gac cat ctg tgg aag tgg gga ttt tac aca cca gac aac aaa yat<br>Arg Asp His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Asn Lys Xaa<br>305 310 315 320 | 960 |

cag aaa gaa cct cca ttc cgt tgg atg ggc tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gat agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

aat tat gca gga 1116  
 Asn Tyr Ala Gly  
 370

<210> 94  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 94  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
 1 5 10 15

ggg caa cta ata gag gct cta ttg gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
 20 25 30

tta gaa gaa atg gat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly  
 35 40 45

gga att gga ggt tgg atc aaa gta aga caa tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Trp Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60

gaa att tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cca gtc aac gta att gga aga aat ctg atg act cag att ggt tgc act 288  
 Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

|   |      |
|---|------|
| aag ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gat ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg tta cca aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Pro Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672  |
| aaa tat act gca ttt acc ata cct agt ata aat aat gag aca cca gga<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| gtt aga tat cag tac aat gtg ctc cca cag ggg tgg aaa gga tca cca<br>Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg acc aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| cag aat cca aac ata ctt att tgt caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asn Ile Leu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg tgg aga tgg ggg ttt tac aca cca gat aaa aaa cat<br>Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gag ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agy cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Xaa Gln<br>355 360 365     | 1104 |
| att tat gca ggg<br>Ile Tyr Ala Gly<br>370   | 1116 |

<210> 95  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 95  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
 1 5 10 15  
 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30  
 tta gaa gaa atg aat ttg cca gga agg tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata tcc gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Val  
 50 55 60  
 gaa atc tgt ggr cat aaa gct ata ggt aca gta tta rta gga cct aca 240  
 Glu Ile Cys Xaa His Lys Ala Ile Gly Thr Val Leu Xaa Gly Pro Thr  
 65 70 75 80  
 cct gtc aac ata att gga agg aat ttg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140  
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175  
 aga gaa ctt aat aag aaa act caa gac ttt tgg gar gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

```

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
      195                                200                                205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
      210                                215                                220

aag tac act gca ttt act ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
      225                                230                                235                                240

att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
      245                                250                                255

gca ata ttc cag tgt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
      260                                265                                270

caa aat cca gar ata gtt atc tat caa tac atg gat gat ctg tat gta      864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
      275                                280                                285

gga tct gac tta gaa ata gaa cag cat aga ata aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ile Lys Ile Glu Glu Leu
      290                                295                                300

aga cac cat ctg ttg aaa tgg gga ttt wmc aca cca gac aaa aaa cat      960
Arg His His Leu Leu Lys Trp Gly Phe Xaa Thr Pro Asp Lys Lys His
      305                                310                                315                                320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325                                330                                335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
      340                                345                                350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                                360                                365

att tac cca ggg
Ile Tyr Pro Gly
      370

```

```

<210> 96
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

<400> 96  
 cct caa atc act ctt tgg caa cga ccc aat gtc aca gta aag ata ggr 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Asn Val Thr Val Lys Ile Xaa  
 1 5 10 15

ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att ggg ggt ttt atc aaa gta aga sag tat gat cag gta ccc gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Xaa Tyr Asp Gln Val Pro Val  
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga ccc aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta ara tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Xaa Leu Lys  
 100 105 110

cca ggr atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Xaa Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe  
 145 150 155 160

gcc ata aag aaa aaa gac ggt act aaa tgg aga aaa gta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Val Val Asp Phe  
 165 170 175

agg gaa ctc aat aag aga act caa gac ttc tgg gaa gtt caa tta ggm 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Xaa  
 180 185 190

ata cca cat ccc gca ggg ttg aaa aag aaa aaa tca gtr aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Xaa Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gaa ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Glu Phe Arg  
 210 215 220

aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly  
 225 230 235 240

atc aga tat caa tac aat gtg ctt cca cag gga tgg aag gga tca cca 768  
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255



|   |      |
|---|------|
| gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gac ata gtc atc tat caa tac gtg gat gat ttg tat gta | 864  |
| Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val |      |
| 275 280 285   |      |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat | 960  |
| Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gta cag cgt ata gag ctg cca gaa aag gag agc tgg act | 1056 |
| Lys Trp Thr Val Gln Arg Ile Glu Leu Pro Glu Lys Glu Ser Trp Thr |      |
| 340 345 350   |      |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa | 1104 |
| Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln |      |
| 355 360 365   |      |
| atw tac cca ggg   | 1116 |
| Xaa Tyr Pro Gly   |      |
| 370   |      |

<210> 97  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|   |     |
|---|-----|
| <400> 97  |     |
| cct caa atc act ctt tgg caa cga ccc ctc gtc aaa ata aag ata ggg | 48  |
| Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Lys Ile Lys Ile Gly |     |
| 1 5 10 15   |     |
| ggg caa ata aag gaa gcy tta tta gat aca gga gca gat gat aca gtg | 96  |
| Gly Gln Ile Lys Glu Xaa Leu Leu Asp Thr Gly Ala Asp Asp Thr Val |     |
| 20 25 30  |     |
| tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa ttg ata ggg | 144 |
| Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly |     |
| 35 40 45  |     |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt ata | 192 |
| Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act<br>Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta cta gaa att tgt aca gaa ctg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Leu Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga act caa gac ttt tgg gag gtt caa cta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gsa ggg tta aga aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Xaa Gly Leu Arg Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gag gac tty agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg<br>210 215 220     | 672 |
| aaa tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att agg tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac ata gtt atc trt caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Xaa Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912 |
| aga caa cat ctg tgg cag tgg gga ttt ttc aca cca gac aaa aaa cat<br>Arg Gln His Leu Trp Gln Trp Gly Phe Phe Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960 |

|   |      |
|---|------|
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp     |      |
| 325 330 335   |      |
| aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag | 1104 |
| Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln |      |
| 355 360 365   |      |
| att tac cca ggg   | 1116 |
| Ile Tyr Pro Gly   |      |
| 370   |      |
| <br><210> 98  |      |
| <211> 1115  |      |
| <212> DNA   |      |
| <213> Human Immunodeficiency Virus (HIV)                        |      |
| <br><220>   |      |
| <221> CDS   |      |
| <222> (1)...(297)   |      |
| <223> HIV Protease  |      |
| <br><221> CDS   |      |
| <222> (298)...(1115)  |      |
| <223> Portion of HIV Reverse Transcriptase                      |      |
| <br><400> 98  |      |
| cct caa atc act ctt tgg caa cga ccc gtc gtc aca ata aag ata ggg | 48   |
| Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Val Thr Ile Lys Ile Gly |      |
| 1 5 10 15   |      |
| ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta | 96   |
| Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val |      |
| 20 25 30  |      |
| tta gaa gaa atg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg | 144  |
| Leu Glu Glu Met His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly |      |
| 35 40 45  |      |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct gta | 192  |
| Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Val |      |
| 50 55 60  |      |
| gaa aty tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca | 240  |
| Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr |      |
| 65 70 75 80   |      |
| cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act | 288  |
| Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr |      |
| 85 90 95  |      |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag | 336  |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |      |
| 100 105 110   |      |
| cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |      |
| 115 120 125   |      |

|   |      |
|---|------|
| aaa ata aaa gca tta gta gaa ata tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cca gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa ttg gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca gga tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gay ata gtt att tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tcc gac cta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cac ctg ttg aag tgg ggr ttt acc ack cca gac aaa aaa cat<br>Arg Gln His Leu Leu Lys Trp Xaa Phe Thr Xaa Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gta ctg cca gaa aaa gat agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tac tca gt<br>Ile Tyr Ser<br>370  | 1115 |

<210> 99  
 <211> 1115  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1115)  
 <223> Portion of HIV Reverse Transcriptase

<400> 99  
 cct cag atc act ctt tgg cag cga ccc ctc gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly  
 1 5 10 15  
 ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30  
 tta gaa gaa atg aat ttg cca gga agr tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggc ttt atc aaa gta aga cag tat gat cag ata ccc cta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Leu  
 50 55 60  
 gaa atc tgt ggc cat aag gct ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80  
 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc att agt cct att gaa act gta cct gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140  
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175  
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

|   |      |
|---|------|
| ata cca cat ccc tca ggg tta raa aag aag aaa tca gta aca gta ctg | 624  |
| Ile Pro His Pro Ser Gly Leu Xaa Lys Lys Lys Ser Val Thr Val Leu |      |
| 195 200 205   |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gat ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg |      |
| 210 215 220   |      |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |      |
| 225 230 235 240   |      |
| att agg tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro |      |
| 245 250 255   |      |
| gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt aga aaa | 816  |
| Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys |      |
| 260 265 270   |      |
| caa aat cca gaa ata gtt atc tac caa tac dtg gat gat ttg tak gta | 864  |
| Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Xaa Val |      |
| 275 280 285   |      |
| rgc tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg | 912  |
| Xaa Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu |      |
| 290 295 300   |      |
| aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat | 960  |
| Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His |      |
| 305 310 315 320   |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp |      |
| 325 330 335   |      |
| aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr |      |
| 340 345 350   |      |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag | 1104 |
| Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln |      |
| 355 360 365   |      |
| att tat gca gg  | 1115 |
| Ile Tyr Ala   |      |
| 370   |      |

&lt;210&gt; 100

&lt;211&gt; 1115

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (297)

&lt;223&gt; HIV Protease

&lt;221&gt; CDS

&lt;222&gt; (298) ... (1115)

&lt;223&gt; Portion of HIV Reverse Transcriptase

|   |     |
|---|-----|
| <400> 100   |     |
| cct caa atc act ctt tgg caa cga ccc cta gtc aca ata aag ata gga<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly<br>1 5 10 15       | 48  |
| ggg cag ctr aag gaa gct ata tta gat aca gga gca gat gat aca kta<br>Gly Gln Xaa Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Asp Thr Xaa<br>20 25 30        | 96  |
| tta gaa gaa atg aat tng ccc gga aga tgg ama cca ama ttg ata ggg<br>Leu Glu Glu Met Asn Xaa Pro Gly Arg Trp Xaa Pro Xaa Leu Ile Gly<br>35 40 45        | 144 |
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gtt ata ggt aca gta ttg gta gga cct aca<br>Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct acc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act<br>Pro Thr Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca ata ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Ile Leu<br>195 200 205     | 624 |
| gat gtg ggc gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672 |
| aaa gta tac tgc ttt acc ata cct agt ata acc aat gag acm cca ggg<br>Lys Val Tyr Cys Phe Thr Ile Pro Ser Ile Thr Asn Glu Xaa Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctg cca caa gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |

gca ata ttc caa agt agc atg aca aaa atc tta gag ccy ttt aga aaa 816  
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Xaa Phe Arg Lys  
260 265 270

caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta 864  
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val  
275 280 285

gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg 912  
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu  
290 295 300

aga caa cat ctg tgg agg tgg gga ttt tac aca cca gac aaa aaa cat 960  
Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His  
305 310 315 320

cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335

aaa tgg aca gta cag cct ata arg ttg cca gaa aaa gac agc tgg act 1056  
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350

gtc aat gam ata cag aaa tta gtg gga aaa tta aat tgg gcc agt cag 1104  
Val Asn Xaa Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
355 360 365

att tck cng gg 1115  
Ile Xaa Xaa  
370

<210> 101  
<211> 1096  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease

<221> CDS  
<222> (298)...(1096)  
<223> Portion of HIV Reverse Transcriptase

<400> 101  
cct car atc act ctt tgg cag acc ccc ctt gtc yca ata agg aka ggg 48  
Pro Gln Ile Thr Leu Trp Gln Thr Pro Leu Val Xaa Ile Arg Xaa Gly  
1 5 10 15

ggr cag yta aag gaa gct tta tta gay aca gra gca gat gat mca gta 96  
Xaa Gln Xaa Lys Glu Ala Leu Leu Asp Thr Xaa Ala Asp Asp Xaa Val  
20 25 30

tta gaa gaa atg tat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
Leu Glu Glu Met Tyr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
35 40 45

gga att gga ggt ttt atc aag gta aga cag tat gat cag ata ccc ata 192  
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
50 55 60



|   |     |
|---|-----|
| gaa atc tgt gga cac aaa gct ata ggt aca gta ttg gta gga tct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr<br>65 70 75 80     | 240 |
| cct gtt aac ata att gga aga aat ctg ttg act cag att ggt tgc acc<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt tct att gaa act gta cca gta aga tta aag<br>Leu Asn Phe Pro Ile Ser Ser Ile Glu Thr Val Pro Val Arg Leu Lys<br>100 105 110     | 336 |
| ccc gga atg gat ggc cca aaa gtt aag caa tgg cca tta aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aag aac agt gat aga tgg aga aaa gta gta gat ttc<br>Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Val Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga acc caa gac ttt tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa agg aga aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Arg Arg Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tac ttt tca att ccc tta gat aaa gaa ttc aga<br>Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga gaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Glu<br>260 265 270     | 816 |
| cag aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu<br>290 295 300     | 912 |
| aga caa cat ctg ttg agg tgg gga tta ttc aca cca gac caa aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Leu Phe Thr Pro Asp Gln Lys His<br>305 310 315 320 | 960 |

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ccg gat 1008  
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
325 330 335

aaa tgg aca gta cag act ata gtg ctg cca gag aag gac agc tgg act 1056  
Lys Trp Thr Val Gln Thr Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  
340 345 350

gtc aat gac ata cag aag tta gta gga aaa ttg aat tgg g 1096  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp  
355 360 365

 $\langle 210 \rangle$  102

<211> 1048

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

 $\langle 220 \rangle$ 

<221> CDS

<222> (1) . . . (297)

<223> HIV Protease

<221> CDS

<222> (298) . . . (1048)

<223> Portion of HIV Reverse Transcriptase

<400> 102

cct cag atc act ctt tgg cag cga ccc tty gtc aca ata aag gta ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Ile Lys Val Gly  
 1 5 10 15

ggg caa cta aag gaa gct cta ttg gat aca gga gca gat gat aca ata 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile  
20 25 30

tta gaa gaa atg tgt ttg cca gga aga tgg aaa cca aaa ttg ata ggg 144  
Leu Glu Glu Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly  
35 40 45

gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata 192  
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
50 55 60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca 240  
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr  
65 70 75 80

cct gcc aac ata gtt gga aga aat ctg ttg act cag att ggc tgt act 288  
Pro Ala Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
100 105 110

cca gga atg gat ggg cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gag aag gat gga 432  
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly  
130 135 140

```

aaa att tca aaa att ggg cct gaa aat cca tay aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145                               150                               155                               160

gcc ata aag aaa aaa aat agt gat aaa tgg aga aaa gta gta gat ttc      528
Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Val Val Asp Phe
                               165                               170                               175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                               180                               185                               190

ata cca cat ccc gga ggg tta rag aag aac aaa tca ata aca gta ctg      624
Ile Pro His Pro Gly Gly Leu Xaa Lys Asn Lys Ser Ile Thr Val Leu
                               195                               200                               205

gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg
                210                               215                               220

aag tat act gca ttt acc ata ccy agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Xaa Ser Ile Asn Asn Glu Thr Pro Gly
225                               230                               235                               240

att aga tat cag tat aat gtg ctt cca cag gga tgg aag gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                               245                               250                               255

gcc ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aag      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                               260                               265                               270

caa aat cca gac ata att atc gtt caa tac gtg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Ile Ile Val Gln Tyr Val Asp Asp Leu Tyr Val
                275                               280                               285

gca tct gac tta gaa ata ggg cag cat aga aca aaa ata aag gaa cta      912
Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Lys Glu Leu
                290                               295                               300

aga caa tat ctg tgg gag tgg gga ttt tac aca cca gag aaa aaa cat      960
Arg Gln Tyr Leu Trp Glu Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                               310                               315                               320

caa cag gaa ccc cca ttc ctc tgg atg ggg tat gag ctc cat cct gat     1008
Gln Gln Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                               325                               330                               335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac a                1048
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp
                340                               345

```

```

<210> 103
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1) ... (297)
<223> HIV Protease

```

&lt;221&gt; CDS

&lt;222&gt; (298) ... (1116)

&lt;223&gt; Portion of HIV Reverse Transcriptase

&lt;400&gt; 103

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cct | cag | atc | act | ctt | tgg | caa | cga | ccc | ctc | gtc | aca | ata | arg | rta | ggg | 48  |
| Pro | Gln | Ile | Thr | Leu | Trp | Gln | Arg | Pro | Leu | Val | Thr | Ile | Xaa | Xaa | Gly |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| ggg | cag | cta | aag | gaa | gct | cta | tta | gat | aca | gga | gca | gat | gat | aca | gta | 96  |
| Gly | Gln | Leu | Lys | Glu | Ala | Leu | Leu | Asp | Thr | Gly | Ala | Asp | Asp | Thr | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| tta | gaa | gaa | atg | aat | ttg | cca | gga | aga | tgg | aaa | cca | aaa | atg | ata | ggg | 144 |
| Leu | Glu | Glu | Met | Asn | Leu | Pro | Gly | Arg | Trp | Lys | Pro | Lys | Met | Ile | Gly |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| gga | att | gga | ggt | ttt | atc | aaa | gta | aga | cag | tat | gat | cag | ata | ccc | ata | 192 |
| Gly | Ile | Gly | Gly | Phe | Ile | Lys | Val | Arg | Gln | Tyr | Asp | Gln | Ile | Pro | Ile |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| gaa | atc | tgt | gga | cat | aaa | gct | gaa | ggt | aca | gta | tta | gta | gga | cct | aca | 240 |
| Glu | Ile | Cys | Gly | His | Lys | Ala | Glu | Gly | Thr | Val | Leu | Val | Gly | Pro | Thr |     |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| ccg | gtc | aac | ata | att | gga | aga | aat | ctg | ttg | act | cag | att | ggt | tgc | act | 288 |
| Pro | Val | Asn | Ile | Ile | Gly | Arg | Asn | Leu | Leu | Thr | Gln | Ile | Gly | Cys | Thr |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| tta | aat | ttt | ccc | att | agt | cct | att | gaa | act | gta | cca | gta | aaa | tta | aag | 336 |
| Leu | Asn | Phe | Pro | Ile | Ser | Pro | Ile | Glu | Thr | Val | Pro | Val | Lys | Leu | Lys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| cca | gga | atg | gat | ggc | cca | aaa | gtt | aaa | caa | tgg | cca | ctg | aca | gaa | gaa | 384 |
| Pro | Gly | Met | Asp | Gly | Pro | Lys | Val | Lys | Gln | Trp | Pro | Leu | Thr | Glu | Glu |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| aaa | ata | aaa | gca | tta | aba | gaa | att | tgt | aca | gaa | atg | gaa | aag | gaa | ggr | 432 |
| Lys | Ile | Lys | Ala | Leu | Xaa | Glu | Ile | Cys | Thr | Glu | Met | Glu | Lys | Glu | Xaa |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| aaa | att | tca | aaa | att | ggg | cct | gaa | aat | cca | tac | aat | act | ccg | gta | ttt | 480 |
| Lys | Ile | Ser | Lys | Ile | Gly | Pro | Glu | Asn | Pro | Tyr | Asn | Thr | Pro | Val | Phe |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| gcc | ata | aag | aaa | aaa | gac | agt | act | aaa | tgg | aga | aaa | tta | gta | gat | ttc | 528 |
| Ala | Ile | Lys | Lys | Lys | Asp | Ser | Thr | Lys | Trp | Arg | Lys | Leu | Val | Asp | Phe |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| aga | gaa | ctt | aat | aag | aaa | act | caa | gac | ttt | tgg | gaa | gtt | caa | tta | gga | 576 |
| Arg | Glu | Leu | Asn | Lys | Lys | Thr | Gln | Asp | Phe | Trp | Glu | Val | Gln | Leu | Gly |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| ata | cca | cac | ccc | gca | ggg | tta | aaa | aag | aaa | aaa | tca | gta | aca | gta | ctg | 624 |
| Ile | Pro | His | Pro | Ala | Gly | Leu | Lys | Lys | Lys | Lys | Ser | Val | Thr | Val | Leu |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| gat | gtg | ggt | gat | gca | tat | ttt | tca | gtt | ccc | tta | gat | aaa | gaa | ttc | agg | 672 |
| Asp | Val | Gly | Asp | Ala | Tyr | Phe | Ser | Val | Pro | Leu | Asp | Lys | Glu | Phe | Arg |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| aag | tat | aca | gca | ttt | acc | ata | cct | agt | aca | aac | aat | gag | aca | ccc | agg | 720 |
| Lys | Tyr | Thr | Ala | Phe | Thr | Ile | Pro | Ser | Thr | Asn | Asn | Glu | Thr | Pro | Arg |     |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |

|   |      |
|---|------|
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tcg cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tat gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gag ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga saa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat<br>Arg Xaa His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gtr cag cct ata rag ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Xaa Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aaa tta gtg gga aaa tta aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tac gca gga<br>Ile Tyr Ala Gly<br>370   | 1116 |

<210> 104  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|  |     |
|--|-----|
| <400> 104<br>cct cag atc act ctt tgg caa cga ccc mty gtc aca ata aag gta ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly<br>1 5 10 15 | 48  |
| ggg caa tta aaa gaa gct cta tta gat aca gga gca gat gat aca gta<br>Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val<br>20 25 30               | 96  |
| cta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg<br>Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly<br>35 40 45               | 144 |

|   |     |
|---|-----|
| gga att gga ggt ttt atc aaa gta aga cag tat gat car ata cyt ata<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile<br>50 55 60        | 192 |
| gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ctg ttr act cag att ggc tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc ata agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gya gaa att tgt aca gaa atg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat cca gca ggg cta cca agg aaa aga tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Pro Arg Lys Arg Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca ccg ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gta ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gcc ata ttc caa agt agc atg aca aaa att tta gat cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| gca tct gac tta gaa ata ggg cag cac aga aca aaa ata gaa gaa cta<br>Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912 |

```

aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                      310                      315                      320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tat gca ggg
Ile Tyr Ala Gly
                      370

<210> 105
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 105
cct cag atc act ctt tgg caa cga ccc ttc gtc gtc gta aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Val Val Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat aat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val
                      20                      25                      30

ttt gaa gac ytg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Phe Glu Asp Xaa Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ctt gta      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Leu Val
                      50                      55                      60

gaa atc tgt gga caa aaa gct ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
65                      70                      75                      80

cct gtc aac ata att gga agg gat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

```

|  |      |
|--|------|
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa  | 384  |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  |      |
| 115 120 125  |      |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg  | 432  |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  |      |
| 130 135 140  |      |
| aar att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt  | 480  |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  |      |
| 145 150 155 160  |      |
| gcc ata aag aaa aaa gac agt act aar tgg aga aaa tta gta gat ttc  | 528  |
| Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  |      |
| 165 170 175  |      |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga  | 576  |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  |      |
| 180 185 190  |      |
| ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg  | 624  |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  |      |
| 195 200 205  |      |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gay' ttc agg | 672  |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg  |      |
| 210 215 220  |      |
| aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca gga  | 720  |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  |      |
| 225 230 235 240  |      |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca  | 768  |
| Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  |      |
| 245 250 255  |      |
| gca ata ttc caa tgt agc atg aca aaa atc tta gat cct ttt aga aag  | 816  |
| Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys  |      |
| 260 265 270  |      |
| caa aat cca gac cta gtt atc tat caa tac rtg gat gac ttg tat gta  | 864  |
| Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Tyr Val  |      |
| 275 280 285  |      |
| gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg  | 912  |
| Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu  |      |
| 290 295 300  |      |
| aga car cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aar cat  | 960  |
| Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His  |      |
| 305 310 315 320  |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat  | 1008 |
| Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  |      |
| 325 330 335  |      |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act  | 1056 |
| Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr  |      |
| 340 345 350  |      |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag  | 1104 |
| Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  |      |
| 355 360 365  |      |



att tac cca ggg  
 ile Tyr Pro Gly  
 370

1116

<210> 106  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 106  
 cct cag atc act ctt ngg caa cga ccm att gtc aca ata aag gta ggg 48  
 Pro Gln Ile Thr Leu Xaa Gln Arg Xaa Ile Val Thr Ile Lys Val Gly  
 1 5 10 15  
 ggg cam tta aaa gaa gtt ytt tta gat mma gga gca gat gat cma gta 96  
 Gly Xaa Leu Lys Glu Val Xaa Leu Asp Xaa Gly Ala Asp Asp Xaa Val  
 20 25 30  
 tta gaa gaa atr gat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Leu Glu Glu Xaa Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata gtt gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Val Val  
 50 55 60  
 gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80  
 cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gag gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140  
 aaa att tca aaa aty ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Xaa Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

|   |      |
|---|------|
| agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat ccc gca ggg yta aaa aag aac aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Xaa Lys Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttc tca gtt ccc tta gat aaa gac ttt agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata ccc agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tat aat gtg ctt cca caa gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt agg aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gaa gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga gca cat ctg tta aag tgg gga ttt acc aca cca gay aaa aag cat<br>Arg Ala His Leu Leu Lys Trp Gly Phe Thr Pro Asp Lys Lys His<br>305 310 315 320     | 960  |
| cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gtg cag cct ata aag ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gcc agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |
| att tat cca gga<br>Ile Tyr Pro Gly<br>370   | 1116 |

&lt;210&gt; 107

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (297)

&lt;223&gt; HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 107

|   |     |
|---|-----|
| cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg | 48  |
| Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly |     |
| 1 5 10 15   |     |
| ggg caa cta aag gaa gct tta tta gat aca gga gca gat gat aca gta | 96  |
| Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val |     |
| 20 25 30  |     |
| tta gaa gaa atg gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg | 144 |
| Leu Glu Glu Met Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly |     |
| 35 40 45  |     |
| gga att gga ggt ttt atc aaa gta agm cag tat gat cag ata ccc ata | 192 |
| Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile |     |
| 50 55 60  |     |
| gaa att tgt gga cat aaa gct gtg ggt aca gta tta gta gga cct aca | 240 |
| Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr |     |
| 65 70 75 80   |     |
| cct gtc aac ata att gga aga aat ctg ttg act aag att ggt tgc act | 288 |
| Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Lys Ile Gly Cys Thr |     |
| 85 90 95  |     |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag | 336 |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys |     |
| 100 105 110   |     |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa | 384 |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |     |
| 115 120 125   |     |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga | 432 |
| Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |     |
| 130 135 140   |     |
| aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt | 480 |
| Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |     |
| 145 150 155 160   |     |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc | 528 |
| Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe |     |
| 165 170 175   |     |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga | 576 |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly |     |
| 180 185 190   |     |
| ata cca cat ccc gca ggg tta aaa mgg aaa aaa tca gta aca gta ctg | 624 |
| Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Lys Ser Val Thr Val Leu |     |
| 195 200 205   |     |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gag ttc agg | 672 |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg |     |
| 210 215 220   |     |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca gga | 720 |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly |     |
| 225 230 235 240   |     |

```

att aga tat cag tac aat gtg yyt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Xaa Pro Gln Gly Trp Lys Gly Ser Pro
                245                250                255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                260                265                270

caa aat cca gaa ata gtt atc tat cag tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                275                280                285

gga tct gac tta gaa ata ggg cag cac aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
                290                295                300

aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                310                315                320

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                325                330                335

aaa tgg aca gta cag cct ata gtg cta cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                340                345                350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355                360                365

att tay gca ggg
Ile Tyr Ala Gly
370

```

```

<210> 108
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

```

```

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 108
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                5                10                15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gtg      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20                25                30

tta gaa gaa atg aat ttg cca ggg aaa tgg aag cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
35                40                45

```

|   |     |
|---|-----|
| gga att gga ggg ttt atc aaa gta agm crg tat gat cag ata ccc ata<br>Gly Ile Gly Gly Phe Ile Lys Val Xaa Xaa Tyr Asp Gln Ile Pro Ile<br>50 55 60        | 192 |
| gaa atc tgt gra cat aaa gct aya ggt aca gta tta ata ggm cct act<br>Glu Ile Cys Xaa His Lys Ala Xaa Gly Thr Val Leu Ile Xaa Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga awt ctg atg act cag att ggg tgc act<br>Pro Val Asn Ile Ile Gly Arg Xaa Leu Met Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly<br>130 135 140     | 432 |
| aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat cct gca ggt tta aaa aag aaa aaa tca gta aca gta cta<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggg gat gca tat ttt tca gtt ccc tta gat gaa aac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asn Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gta ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa tgt agc atg aca aaa atc tta gag cct ttc aga aag<br>Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gaa atg gtt atc trc caa tac gtg gat gay ttg tat gta<br>Gln Asn Pro Glu Met Val Ile Xaa Gln Tyr Val Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| ggt tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctr<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Xaa<br>290 295 300     | 912 |

```

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
305                      310                      315                      320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctm cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Xaa His Pro Asp
                      325                      330                      335

aaa tgg aca gtg cag cat ata gaa ctg cca gaa caa gag agc tgg act      1056
Lys Trp Thr Val Gln His Ile Glu Leu Pro Glu Gln Glu Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa yta aat tgg gca agy cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Xaa Gln
                      355                      360                      365

att tat gca ggg
Ile Tyr Ala Gly
370

<210> 109
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 109
cct caa atc act ctt tgg caa cga ccc atc gtc aca gta aag ata gag      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Val Lys Ile Glu
1                      5                      10                      15

ggg cag cta aag gaa gct yta tta gat aca gga gca gat aat aca gta      96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asn Thr Val
                      20                      25                      30

ttg gam gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Xaa Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gra ggt ttt atc aaa gta aam cag tat gat sag ata mcc ata      192
Gly Ile Xaa Gly Phe Ile Lys Val Xaa Gln Tyr Asp Xaa Ile Xaa Ile
50                      55                      60

gac atc tgt gga cat aaa gta ata ggt aca ata tta gta gga cct aca      240
Asp Ile Cys Gly His Lys Val Ile Gly Thr Ile Leu Val Gly Pro Thr
65                      70                      75                      80

cct gtc aac ata att gga aga gat ctg ttg act cag att ggc tgc act      288
Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

```

|   |      |
|---|------|
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gar gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432  |
| aag att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat tty tca gtt ccc tta gmt aaa gaa tnn nnn<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Xaa Lys Glu Xaa Xaa<br>210 215 220     | 672  |
| nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn<br>Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa<br>225 230 235 240         | 720  |
| nnn nnn nnn nnn nnn nnn nnn nnn cca cag gga tgg aaa gga tca cca<br>Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gaa ata gtt atc tac car tac rtg gat gay ttg ttw gta<br>Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Xaa Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat<br>Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggy tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |

att tat cca ggg  
 ile Tyr Pro Gly  
 370

1116

&lt;210&gt; 110

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(297)

&lt;223&gt; HIV Protease

&lt;221&gt; CDS

&lt;222&gt; (298)...(1116)

&lt;223&gt; Portion of HIV Reverse Transcriptase

&lt;400&gt; 110

cyt cag atc act ctt tgg caa cga ccc cts gtc aca ata aag gta ggg 48  
 Xaa Gln ile Thr Leu Trp Gln Arg Pro Xaa Val Thr ile Lys Val Gly  
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa atr aat ttg cca ggr aaa tgg aaa cca awa atg ata ggg 144  
 Leu Glu Glu Xaa Asn Leu Pro Xaa Lys Trp Lys Pro Xaa Met ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata 192  
 Gly ile Gly Gly Phe ile Lys Val Arg Gln Tyr Asp Gln ile Leu ile  
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca 240  
 Glu ile Cys Gly His Lys Ala ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn ile ile Gly Arg Asn Leu Leu Thr Gln ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro ile Ser Pro ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca ggg atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta ata gaa atc tgt aca gaa atg gaa aag gaa gga 432  
 Lys ile Lys Ala Leu ile Glu ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys ile Ser Lys ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175



aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gtg aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg  
 210 215 220

aag tac act gca ttt mcc ata cct agt ata aac aat gag aca cca ggg 720  
 Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240

att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca 768  
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816  
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
 260 265 270

caa mat cca gac atg gty atc tat caa tac atg gat gat ttg tat gta 864  
 Gln Xaa Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val  
 275 280 285

gga tct gac tta gaa ata ggr cag cat aga gca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Xaa Gln His Arg Ala Lys Ile Glu Glu Leu  
 290 295 300

aga cag cat ttg ttg aag tgg gga ttt acc aca cca gac aaa aag cat 960  
 Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His  
 305 310 315 320

cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat 1008  
 Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp  
 325 330 335

aaa tgg aca gta cag cct ata gag ctg cca gaa aar gam agc tgg act 1056  
 Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Xaa Ser Trp Thr  
 340 345 350

gtc aat gac ata cag aaa ata gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Ile Val Gly Lys Leu Asn Trp Ala Ser Gln  
 355 360 365

att tac cca ggg 1116  
 Ile Tyr Pro Gly  
 370

<210> 111  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1) ... (297)  
 <223> HIV Protease

&lt;221&gt; CDS

&lt;222&gt; (298)...(1116)

&lt;223&gt; Portion of HIV Reverse Transcriptase

&lt;400&gt; 111

|   |     |
|---|-----|
| cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg | 48  |
| Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly |     |
| 1 5 10 15   |     |
| ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta | 96  |
| Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val |     |
| 20 25 30  |     |
| tta gaa gaa atg agc ttg cca gga aaa tgg aaa cca aaa atg ata ggg | 144 |
| Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly |     |
| 35 40 45  |     |
| gga att gga ggt ttt atc aaa gta agm cag tat gwt cat ata ccc ata | 192 |
| Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Xaa His Ile Pro Ile |     |
| 50 55 60  |     |
| gaa wtc tgt ggm cat aaa gct gaa ggt aca gta tta ata gga cct aca | 240 |
| Glu Xaa Cys Xaa His Lys Ala Glu Gly Thr Val Leu Ile Gly Pro Thr |     |
| 65 70 75 80   |     |
| cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act | 288 |
| Pro Val Asn Ile Ile Gly Arg Asn Leu Thr Gln Leu Gly Cys Thr     |     |
| 85 90 95  |     |
| tta aat ttt ccc ata agt cct att gaa act gta cca gta aga cta aaa | 336 |
| Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Arg Leu Lys |     |
| 100 105 110   |     |
| cca gga atg gat ggg cca aaa gtt aag caa tgg cca cta aca gaa gaa | 384 |
| Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu |     |
| 115 120 125   |     |
| aaa atc aaa gca ttg ata gaa att tgt aca gaa atg gaa aag gaa gga | 432 |
| Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly |     |
| 130 135 140   |     |
| aaa att gaa aaa att ggg cct gaa aat cca tac aat act cca gta ttt | 480 |
| Lys Ile Glu Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe |     |
| 145 150 155 160   |     |
| gcc ata agg aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc | 528 |
| Ala Ile Arg Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe |     |
| 165 170 175   |     |
| aga gaa ctt aat aag aga act caa gac ttt tgg gaa att caa tta gga | 576 |
| Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly |     |
| 180 185 190   |     |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg | 624 |
| Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu |     |
| 195 200 205   |     |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg | 672 |
| Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg |     |
| 210 215 220   |     |
| aag tat act gca ttt acc ata cct agt gta aat aat gag aca cca gga | 720 |
| Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly |     |
| 225 230 235 240   |     |

```

att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                245                250                255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
                260                265                270

caa aat cca gaa yta gtt atc tac caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Glu Xaa Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val
                275                280                285

gga tca gac tta gaa ata gar aag cat aga gca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Lys His Arg Ala Lys Ile Glu Glu Leu
                290                295                300

aga gaa cat ctg tya aaa tgg ggg ttt acc aca cca gac aaa aaa cat      960
Arg Glu His Leu Xaa Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His
                305                310                315                320

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                325                330                335

aaa tgg aca gta cag acc ata aag ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Thr Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr
                340                345                350

gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                355                360                365

att tat cca ggg
Ile Tyr Pro Gly
                370

```

```

<210> 112
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

```

```

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

```

```

<400> 112
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1                5                10                15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20                25                30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atk ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly
                35                40                45

```

|   |     |
|---|-----|
| gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta<br>Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val<br>50 55 60        | 192 |
| gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca<br>Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr<br>65 70 75 80     | 240 |
| cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act<br>Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr<br>85 90 95        | 288 |
| tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag<br>Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys<br>100 105 110     | 336 |
| cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384 |
| aaa ata aaa gca tta atg gaa att tgt gca gaa wtg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Glu Xaa Glu Lys Glu Gly<br>130 135 140     | 432 |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480 |
| gcc ata aag aaa aaa gac agc act aaa tgg ara aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Xaa Lys Leu Val Asp Phe<br>165 170 175     | 528 |
| aga gaa ctt aat aar aga act caa gac ttt tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576 |
| ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624 |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg<br>210 215 220     | 672 |
| aag tat act gca ttt acc ata cct agt ata aac aat gag acm cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly<br>225 230 235 240 | 720 |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768 |
| gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816 |
| caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864 |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912 |

```

aga cag cat ctg ttg aag tgg gga ttk tmc aca cca gac aaa aaa cat      960
Arg Gln His Leu Leu Lys Trp Gly Xaa Xaa Thr Pro Asp Lys Lys His
305                      310                      315                      320

cag aaa saa cct cca ttc ctt tgg atg ggt tat gaa ctc cmt cct gat      1008
Gln Lys Xaa Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu Xaa Pro Asp
                      325                      330                      335

aaa tgg aca gta caa cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa ttr aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln
                      355                      360                      365

att tac gca ggg
Ile Tyr Ala Gly
370

<210> 113
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 113
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
50                      55                      60

gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca      240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr
65                      70                      75                      80

cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

```

|   |      |
|---|------|
| cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg acm gaa gaa<br>Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Xaa Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta ata gaa atc tgc aca gaa atg gaa aag gam sga<br>Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Xaa Xaa<br>130 135 140     | 432  |
| waa att tca aaa mta ggg cct gam wat cca tac aat act cca gta ttt<br>Xaa Ile Ser Lys Xaa Gly Pro Xaa Xaa Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cac ccg gca ggg tta aaa aag aac aaa tca gta aca gtg ttg<br>Ile Pro His Pro Ala Gly Leu Lys Asn Lys Ser Val Thr Val Leu<br>195 200 205         | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gag ttc agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg<br>210 215 220     | 672  |
| aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa tst agc atg aca aaa atc tta gag cct ttt aga aaa<br>Ala Ile Phe Gln Xaa Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ttg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga gaa cat ctg ttg aag tgg gga ttt acc aca cca gat aaa aaa cat<br>Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gag ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |

att tat gca ggg  
Ile Tyr Ala Gly  
370

1116

<210> 114  
<211> 1116  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
<221> CDS  
<222> (1)...(297)  
<223> HIV Protease

<221> CDS  
<222> (298)...(1116)  
<223> Portion of HIV Reverse Transcriptase

<400> 114  
cmt caa atm amt ctt tgg car mra ccc cta gtc cna awn nmm gkk agg 48  
Xaa Gln Xaa Xaa Leu Trp Gln Xaa Pro Leu Val Xaa Xaa Xaa Xaa Arg  
1 5 10 15  
ggg gca aat aag gaa gct cta tta gac aca gga gca gat gat mca gta 96  
Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Xaa Val  
20 25 30  
tta gaa gaa atg wat tta cca gga aaa tgg aaa cca aaa atg ata ggg 144  
Leu Glu Glu Met Xaa Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
35 40 45  
gga att gga ggt ttt atc aaa gta agn cag tat gag cag ata ccc ata 192  
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Glu Gln Ile Pro Ile  
50 55 60  
gaa atc tgt gga cat aaa gct ata ggt aca gta ttg gta ggm cct aca 240  
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr  
65 70 75 80  
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95  
tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
100 105 110  
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa 384  
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
115 120 125  
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg 432  
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
130 135 140  
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
145 150 155 160  
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
165 170 175

```

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
      180                                185                                190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gtg ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
      195                                200                                205

gac gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
      210                                215                                220

aag tat act gca ttt tcy ata cct agt aca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
      225                                230                                235                                240

agt agg tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ser Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
      245                                250                                255

gca ata ttc caa agt agc atg ata aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Ile Lys Ile Leu Glu Pro Phe Arg Lys
      260                                265                                270

caa aat cca raa att gtg atc tat cma tac mtg gat gat ttg tat gta      864
Gln Asn Pro Xaa Ile Val Ile Tyr Xaa Tyr Xaa Asp Asp Leu Tyr Val
      275                                280                                285

gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu
      290                                295                                300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
      305                                310                                315                                320

cag aar gaa cct ccg ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325                                330                                335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac ags ttg rct      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Xaa Leu Xaa
      340                                345                                350

kca aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                                360                                365

att tac tca ggg
Ile Tyr Ser Gly
      370

```

&lt;210&gt; 115

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(297)

&lt;223&gt; HIV Protease



&lt;221&gt; CDS

&lt;222&gt; (298)...(1116)

&lt;223&gt; Portion of HIV Reverse Transcriptase

&lt;400&gt; 115

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| cct | cag | atc | act | ctt | tgg | caa | cga | ccc | ctc | gtc | aca | ata | aag | ata | ggg | 48 |
| Pro | Gln | Ile | Thr | Leu | Trp | Gln | Arg | Pro | Leu | Val | Thr | Ile | Lys | Ile | Gly |    |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ggg | cag | cta | aag | gaa | gct | cta | ata | gat | aca | gga | gca | gat | gat | aca | gtg | 96 |
| Gly | Gln | Leu | Lys | Glu | Ala | Leu | Ile | Asp | Thr | Gly | Ala | Asp | Asp | Thr | Val |    |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | gaa | gaa | atg | agt | ata | cca | gga | aaa | tgg | aaa | cca | aaa | ttg | ata | ggg | 144 |
| Leu | Glu | Glu | Met | Ser | Ile | Pro | Gly | Lys | Trp | Lys | Pro | Lys | Leu | Ile | Gly |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gga | att | gga | ggt | ttt | atc | aaa | gta | aga | cag | tat | gat | cag | gkg | ccc | gta | 192 |
| Gly | Ile | Gly | Gly | Phe | Ile | Lys | Val | Arg | Gln | Tyr | Asp | Gln | Xaa | Pro | Val |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | att | tgt | gga | cat | aaa | gct | ata | ggt | mca | gtw | tta | ata | ggm | cct | aca | 240 |
| Glu | Ile | Cys | Gly | His | Lys | Ala | Ile | Gly | Xaa | Xaa | Leu | Ile | Xaa | Pro | Thr |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cct | gcc | aac | ata | att | gga | agg | aat | ctg | ttg | act | cag | att | ggt | tgc | act | 288 |
| Pro | Ala | Asn | Ile | Ile | Gly | Arg | Asn | Leu | Leu | Thr | Gln | Ile | Gly | Cys | Thr |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | aat | ttt | ccc | att | agt | cct | att | gaa | act | gta | cca | gta | aaa | tta | aag | 336 |
| Leu | Asn | Phe | Pro | Ile | Ser | Pro | Ile | Glu | Thr | Val | Pro | Val | Lys | Leu | Lys |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cca | gga | atg | gat | ggc | cca | aaa | ggt | aag | caa | tgg | cca | ttg | aca | gaa | gag | 384 |
| Pro | Gly | Met | Asp | Gly | Pro | Lys | Val | Lys | Gln | Trp | Pro | Leu | Thr | Glu | Glu |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | ata | aaa | gca | tta | aca | gaa | att | tgt | aca | gaa | atg | gaa | aag | gaa | gga | 432 |
| Lys | Ile | Lys | Ala | Leu | Thr | Glu | Ile | Cys | Thr | Glu | Met | Glu | Lys | Glu | Gly |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aag | att | tca | aaa | att | ggg | cct | gaa | aat | cca | tac | aat | act | cca | gta | ttt | 480 |
| Lys | Ile | Ser | Lys | Ile | Gly | Pro | Glu | Asn | Pro | Tyr | Asn | Thr | Pro | Val | Phe |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gcc | ata | aag | aaa | aaa | gac | agt | act | aaa | tgg | aga | aaa | tta | gta | gat | ttc | 528 |
| Ala | Ile | Lys | Lys | Lys | Asp | Ser | Thr | Lys | Trp | Arg | Lys | Leu | Val | Asp | Phe |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aga | gaa | ctt | aat | aag | aga | act | caa | gat | ttc | tgg | gaa | gtt | caa | tta | gga | 576 |
| Arg | Glu | Leu | Asn | Lys | Arg | Thr | Gln | Asp | Phe | Trp | Glu | Val | Gln | Leu | Gly |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ata | cca | cat | cct | gca | ggg | tta | aaa | aag | aaa | aaa | tca | gta | aca | gta | ctg | 624 |
| Ile | Pro | His | Pro | Ala | Gly | Leu | Lys | Lys | Lys | Lys | Ser | Val | Thr | Val | Leu |     |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gat | gtg | ggt | gat | gca | tat | ttt | tca | gtt | ccc | tta | gat | gaa | gac | ttt | agg | 672 |
| Asp | Val | Gly | Asp | Ala | Tyr | Phe | Ser | Val | Pro | Leu | Asp | Glu | Asp | Phe | Arg |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | tat | act | gca | ttt | acc | ata | cct | agt | gta | aac | aat | gag | aca | cca | ggg | 720 |
| Lys | Tyr | Thr | Ala | Phe | Thr | Ile | Pro | Ser | Val | Asn | Asn | Glu | Thr | Pro | Gly |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |

|  |      |
|--|------|
| att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro | 768  |
| 245 250 255  |      |
| gca ata ttc caa tgt agt atg aca aaa ata tta gag ccc ttt aga aaa<br>Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys | 816  |
| 260 265 270  |      |
| caa aat cca gac cta gtt atc tat caa tac gtg gat gat ttg tat gta<br>Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val | 864  |
| 275 280 285  |      |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu | 912  |
| 290 295 300  |      |
| aga caa cat ctg ttg aaa tgg ggt ttt acc aca cca gac aaa aag cat<br>Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His | 960  |
| 305 310 315 320  |      |
| cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp | 1008 |
| 325 330 335  |      |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr | 1056 |
| 340 345 350  |      |
| gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln | 1104 |
| 355 360 365  |      |
| att tac cca ggg<br>Ile Tyr Pro Gly   | 1116 |
| 370  |      |

<210> 116  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (1)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

|  |     |
|--|-----|
| <400> 116  |     |
| cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg<br>Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly | 48  |
| 1 5 10 15  |     |
| ggg cag cta aag gaa gct cta tta gat aca gga gca gat gac aca gta<br>Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val | 96  |
| 20 25 30   |     |
| tta gaa gaa ata agt ctg cca gga aga tgg aaa cca aaa ttg ata ggg<br>Leu Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly | 144 |
| 35 40 45   |     |

gga att gga ggt ttt atc aaa gta aag cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta ggm cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr  
 65 70 75 80

cct gtc aac ata gtt gga aga aat ctg ttg act cag ctt ggt tgc act 288  
 Pro Val Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aag gtt aag caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcc ata aag aaa aaa gac agt aca aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aga act caa gac ttt tgg gaa gtt caa cta ggg 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat aaa gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg  
 210 215 220

aag tac act gca ttt acc ata cct agt ata aat aat gag aca cca ggg 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240

att aga tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816  
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys  
 260 265 270

caa aat cca gac ata gtt atc tat caa tac gta gat gac ttg tat gta 864  
 Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val  
 275 280 285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg 912  
 Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu  
 290 295 300

```

aga caa cat ctg tgg aag tgg ggg ttt tac aca cca gat aaa aaa cat      960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His
305                      310                      315                      320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
                      325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
                      340                      345                      350

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
                      355                      360                      365

att tac cca ggg
Ile Tyr Pro Gly
                      370

<210> 117
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (1)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1119)
<223> Portion of HIV Reverse Transcriptase

<400> 117
cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
1                      5                      10                      15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                      20                      25                      30

tta gaa gaa atg gat ttg cca gga aga tgg aca cca aaa atg ata ggg      144
Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly
                      35                      40                      45

gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50                      55                      60

gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr
65                      70                      75                      80

cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
                      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100                      105                      110

```

|   |      |
|---|------|
| cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa<br>Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu<br>115 120 125     | 384  |
| aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga<br>Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly<br>130 135 140     | 432  |
| aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt<br>Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe<br>145 150 155 160 | 480  |
| gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc<br>Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe<br>165 170 175     | 528  |
| aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga<br>Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly<br>180 185 190     | 576  |
| ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg<br>Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu<br>195 200 205     | 624  |
| gat gtg ggt gat gca tat ttt tca gtt ccc tta gac aag gac ttt agg<br>Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg<br>210 215 220     | 672  |
| aaa tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg<br>Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly<br>225 230 235 240 | 720  |
| att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca<br>Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro<br>245 250 255     | 768  |
| gca ata ttc caa agc agc atg aca aaa atc tta gat cct ttt aga aag<br>Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys<br>260 265 270     | 816  |
| caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta<br>Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val<br>275 280 285     | 864  |
| gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg<br>Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu<br>290 295 300     | 912  |
| aga gaa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat<br>Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His<br>305 310 315 320 | 960  |
| cag aaa gaa cct ccg ttc ctc tgg atg ggt tat gaa ctc cat cct gat<br>Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp<br>325 330 335     | 1008 |
| aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act<br>Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr<br>340 345 350     | 1056 |
| gtc aat gac ata cag aag tta gtg gga aaa ttg aac tgg gca agt cag<br>Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln<br>355 360 365     | 1104 |

att tat yca ggg att  
 Ile Tyr Xaa Gly Ile  
 370

1119

<210> 118  
 <211> 979  
 <212> PRT  
 <213> Human Immunodeficiency Virus

<400> 118  
 Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met  
 1 5 10 15  
 Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys  
 20 25 30  
 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser  
 35 40 45  
 Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys  
 50 55 60  
 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu  
 65 70 75 80  
 Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His  
 85 90 95  
 Pro Ala Gly Leu Lys Gln Lys Lys Ser Val Thr Ile Leu Asp Val Gly  
 100 105 110  
 Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr Thr  
 115 120 125  
 Ala Phe Thr Ile Pro Ser Arg Asn Asn Glu Thr Pro Gly Ile Arg Tyr  
 130 135 140  
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe  
 145 150 155 160  
 Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro  
 165 170 175  
 Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp  
 180 185 190  
 Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Gly His  
 195 200 205  
 Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu  
 210 215 220  
 Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr  
 225 230 235 240  
 Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp  
 245 250 255  
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala  
 260 265 270  
 Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala  
 275 280 285  
 Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala  
 290 295 300  
 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp  
 305 310 315 320  
 Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln  
 325 330 335  
 Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly  
 340 345 350  
 Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu  
 355 360 365  
 Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly  
 370 375 380  
 Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr  
 385 390 395 400  
 Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe  
 405 410 415

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Pro | Pro | Leu | Val | Lys | Leu | Trp | Tyr | Gln | Leu | Glu | Lys | Glu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Pro | Ile | Val | Gly | Ala | Glu | Thr | Phe | Tyr | Val | Asp | Gly | Ala | Ala | Asn | Arg |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Thr | Lys | Leu | Gly | Lys | Ala | Gly | Tyr | Val | Thr | Asn | Arg | Gly | Arg | Gln |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Lys | Val | Val | Thr | Leu | Thr | Asp | Thr | Thr | Asn | Gln | Lys | Thr | Glu | Leu | Gln |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ala | Ile | Tyr | Leu | Ala | Leu | Gln | Asp | Ser | Gly | Leu | Glu | Val | Asn | Ile | Val |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Thr | Asp | Ser | Gln | Tyr | Ala | Leu | Gly | Ile | Ile | Gln | Ala | Gln | Pro | Asp | Gln |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Ser | Glu | Ser | Glu | Leu | Val | Asn | Gln | Ile | Ile | Glu | Gln | Leu | Ile | Lys | Lys |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Glu | Lys | Val | Tyr | Leu | Ala | Trp | Val | Pro | Ala | His | Lys | Gly | Ile | Gly | Ser |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Pro | Ile | Glu | Thr | Val | Pro | Val | Lys | Leu | Lys | Pro | Gly | Met | Asp | Gly | Pro |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Lys | Val | Lys | Gln | Trp | Pro | Leu | Thr | Glu | Glu | Lys | Ile | Lys | Ala | Leu | Val |
|     |     |     | 565 |     |     |     |     | 570 |     |     |     |     |     | 575 |     |
| Glu | Ile | Cys | Thr | Glu | Met | Glu | Lys | Glu | Gly | Lys | Ile | Ser | Lys | Ile | Gly |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Pro | Glu | Asn | Pro | Tyr | Asn | Thr | Pro | Ile | Phe | Ala | Ile | Lys | Lys | Lys | Asp |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ser | Thr | Lys | Trp | Arg | Lys | Leu | Val | Asp | Phe | Arg | Glu | Leu | Asn | Lys | Arg |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Thr | Gln | Asp | Phe | Trp | Glu | Val | Gln | Leu | Gly | Ile | Pro | His | Pro | Ala | Gly |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Leu | Lys | Gln | Lys | Lys | Ser | Val | Thr | Ile | Leu | Asp | Val | Gly | Asp | Ala | Tyr |
|     |     |     | 645 |     |     |     |     |     | 650 |     |     |     |     | 655 |     |
| Phe | Ser | Val | Pro | Leu | Asp | Glu | Gly | Phe | Arg | Lys | Tyr | Thr | Ala | Phe | Thr |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| Ile | Pro | Ser | Arg | Asn | Asn | Glu | Thr | Pro | Gly | Ile | Arg | Tyr | Gln | Tyr | Asn |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
| Val | Leu | Pro | Gln | Gly | Trp | Lys | Gly | Ser | Pro | Ala | Ile | Phe | Gln | Ser | Ser |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |
| Met | Thr | Arg | Ile | Leu | Glu | Pro | Phe | Arg | Lys | Gln | Asn | Pro | Glu | Ile | Val |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Ile | Tyr | Gln | Tyr | Met | Asp | Asp | Leu | Tyr | Val | Gly | Ser | Asp | Leu | Glu | Ile |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     |     | 735 |     |
| Gly | Gln | His | Arg | Ala | Lys | Ile | Glu | Glu | Leu | Arg | Gly | His | Leu | Leu | Lys |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |
| Trp | Gly | Phe | Thr | Thr | Pro | Asp | Lys | Lys | His | Gln | Lys | Glu | Pro | Pro | Phe |
|     |     | 755 |     |     |     |     | 760 |     |     |     |     | 765 |     |     |     |
| Leu | Trp | Met | Gly | Tyr | Glu | Leu | His | Pro | Asp | Lys | Trp | Thr | Val | Gln | Pro |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |
| Ile | Lys | Leu | Pro | Glu | Lys | Asp | Ser | Trp | Thr | Val | Asn | Asp | Ile | Gln | Lys |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |
| Leu | Val | Gly | Lys | Leu | Asn | Trp | Ala | Ser | Gln | Ile | Tyr | Ala | Gly | Ile | Lys |
|     |     |     | 805 |     |     |     |     |     | 810 |     |     |     |     | 815 |     |
| Val | Arg | Gln | Leu | Cys | Lys | Leu | Leu | Arg | Gly | Thr | Lys | Ala | Leu | Thr | Glu |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |
| Val | Ile | Pro | Leu | Thr | Glu | Glu | Ala | Glu | Leu | Glu | Leu | Ala | Glu | Asn | Arg |
|     |     | 835 |     |     |     |     | 840 |     |     |     |     | 845 |     |     |     |
| Glu | Ile | Leu | Lys | Glu | Pro | Val | His | Gly | Val | Tyr | Tyr | Asp | Pro | Ser | Lys |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |
| Asp | Leu | Ile | Ala | Glu | Ile | Gln | Lys | Gln | Gly | Gln | Gly | Gln | Trp | Thr | Tyr |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |
| Gln | Ile | Tyr | Gln | Glu | Pro | Phe | Lys | Asn | Leu | Lys | Thr | Gly | Lys | Tyr | Ala |
|     |     |     | 885 |     |     |     |     |     | 890 |     |     |     |     | 895 |     |
| Arg | Met | Arg | Gly | Ala | His | Thr | Asn | Asp | Val | Lys | Gln | Leu | Thr | Glu | Ala |
|     |     |     | 900 |     |     |     |     | 905 |     |     |     |     | 910 |     |     |
| Val | Gln | Lys | Ile | Thr | Thr | Glu | Ser | Ile | Val | Ile | Trp | Gly | Lys | Thr | Pro |
|     |     | 915 |     |     |     |     | 920 |     |     |     |     | 925 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Phe | Lys | Leu | Pro | Ile | Gln | Lys | Glu | Thr | Trp | Glu | Thr | Trp | Trp | Thr |
|     | 930 |     |     |     |     | 935 |     |     |     |     | 940 |     |     |     |     |
| Glu | Tyr | Trp | Gln | Ala | Thr | Trp | Ile | Pro | Glu | Trp | Glu | Phe | Val | Asn | Thr |
| 945 |     |     |     |     | 950 |     |     |     |     | 955 |     |     |     |     | 960 |
| Pro | Pro | Leu | Val | Lys | Leu | Trp | Tyr | Gln | Leu | Glu | Lys | Glu | Pro | Ile | Val |
|     |     |     |     | 965 |     |     |     |     | 970 |     |     |     |     | 975 |     |
| Gly | Ala | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |